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gene
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                                                                                                                                                                                                                                                                                        gene
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SMSSIVECLLALKDNVATQLGGHISNSTAKTPIRKLELETDGFVLSVATPGKRYPK
SQQRSPLJSQQKINEVVQFWGTYTDLFAKIGENTHANNSLIKTREDKYRKVROILD
ESIERKRGEIPHRVVHLLRNVICEIEHRIGIQADHIRNONSIIKTREDKYRKKIALE
TLVNGTNEERBAAINHLEVVKYEKSKLDEKRKLGEQDMATLIREKENAEMIIASLHQE
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QDGKLTAIDYICENGEILIANPSKQGKEGYRMFKHOEVGELKSQIRVFRPFLPG
QDGKLTAIDYICENGEILIANPSKQGKEGYRMFKHOEVGTHSSQAEVFSDIQPLIRS
VLDGFNVCIFAYGQTGSGKTYTMSGPGTSREDWGVNYRALNDLFDISLSRKNAFSYES
NRAVGSTALNEESSRSHSILTVUVRGLDVKNGSTSGGCHLIDLAGSERVERSEATGD
RLKEAQHINKSLSALGDVTFSLAQKNAHVPYRNSKLTQVLQSSLGQAKTLHTVQINP
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GVERNAFEDNSANDGROSNLLRQSTSSTGLEBVATTIESTICKGNAFGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(1922. 19261,19694. 19848,19915. 20022,20628. 2083;
21203. 21300,21397. 21480,21572. 21649,21807. 21899,
21991. 22020,22277. 22421,22872. 22967,23073. 23252,
23347. 23453,23552. 23653,23956. 24011,24094. 24347,
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join(8072. .8086,9178. .9387,9474. .9671,12990.

14072. .14144,14960. .15376)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(16191. .16218,17138. .17280)
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join(8072 ... 8086, 9178 ... 9387, 9474 ... 9671, 12990 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWCCCFGPAPPAGAREVRPPRLTWPPRRHPGCPATTPSRHRGLDDPPRHGLAPGGQAE
RRPPPPRPGRPRRAAAIRRLRPPLTNKLYAEPQLSAASAPVPGRPSRSRPPPRRLATG
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                                                                                                                                                                                                                                                                                                                                                  SVEAEAEDNASDDGCSVGETEYSPAGASETSAERAYVLILFSFISCAKPSCACDTSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRRRGEDDMSVIR"
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                                                                                                                                                                                                                                                                                                                      LMIVPVRLRTGT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MAITVEWNGQPPSVGHCCIMRPSDVAATCRVQACSCITAAPGGT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                        .29152,29378.
                                                                                                                                                                                                                                    .29152,29378.
                                                                                                                                                                                                                                                                                           .29650)
                                                                                                                                                                                                                                       . 29650)
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AC115717
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      VERSION
                              ACCESSION
                                                                                        DEFINITION
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Best Local S
Matches 21
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pieces.
AC115717
AC115717.3
                                                                                        Mus musculus
                                                                                                                   AC115717
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3 ATATATATCTACATTCAAAACA 24
ATATATATCTACATTCATAACA
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WQVYKALIGGHGVPRVHYKGRQGEYYUIVMTPHEDYYERUCTELALSKILINLYYEKS
TKWRDASTGLHYDYDQRPDVFREFVEYVVNLKFDEEPNYKCISLEDTVVGPNPDIRP
INTDGAGKLHHLVGOKRGRLLMEETDBQPKKKIRMGPLATGWISYYNARRPMKQRYHY
NVADSRLVQHIDKGNEDGLFISCITSCSNLWALIMDAGTGFTSQYYELSPHFLHKEWI
MDQWERNYYITALAGANNGSSLVWASKOTMYTQQSYKVELDFLYPSEGIHQRWDNGY
RITAYAATWDQAAFTLLSVPRKRETDEFDCTLRFSAFPSQHVKXSGHLVEAISSSRLLA
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/gene="OSUNBA0014K08.7"
/gene="OSUNBA0014K08.7"
/gene="OSUNBA0014K08.7"
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(31081. .31242,31391. .31579,31787. .31815, 31903. .31993,32132. .32306,32410. .32549,32638. .32770, 33508. .33574,34086. .34243,34332. .34405,34498. .34609,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAGADTNGSLLCIRKHRRRQDDRSGGASGPIRHDDÏLRMLVRSSRCSRALALHLCPGA
SAFHIFSRRGWSRFRPMDGAVVVTVGDQLQACNGGLYKSVAGKPAYSNDDLRGNGGDT
GVASAELFYCFPSAGTAAGKASEVLSADAGKIIPLNLQFMVAACLVLGYHFLLSSLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(31081..31242,31391..31579,31787..31815,
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33508..33574,34086..34243,34332..34405,34496..34609,
35132..35437))
                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(47169. 47198,47300. 47377,47591. 47689,
47772. 47834,48987. 49058,49145. 49219,49310. 49366,
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/note="hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAC05583.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMWWSPGDGGQEMAGNWALQSGASHFRNTADALFIQLEQTATKIMDVLQRGGAVATQS
                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein similar to Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="OSJNBa0014K08.6"
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                                                                                                                                                                    95.5%;
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                                                                                                                                                                    Score
Pred.
                                                                                                                                       Mismatches
   92812
                                                                                                                                                                        20.4;
No. 2
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2.1e+02;
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226726 bp RP23-28P10, I

DOP DNA

linear HTG 26-JUN-2002 DRAFT SEQUENCE, 9 ordered

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Matches
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                                                                                                                                                      Local
                                           60289
                                                                                   4 TATATATCTACATTCAAAACAA 25
                                                                                                                                                      Similarity
                                           TGTATATCTACATTCAAAACAA 60268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: 6546. .6898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: 6229. .6703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:AQ321209" 6212. .6775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTR16A repeat: matches 6212. .6878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: 5702. .5976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: 6546. .6739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: 6546. .6741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: 6397. .6873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: 6329. .6686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: 6256. .6733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6216.
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/note="LTR16A repeat: matches 132. /note="LTR16A repeat: matches 132. .428 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8497. .8643
/note="L1PB1 repeat: matches 6008.
L1PB1 repeat: matches 6008. .6155 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MER65A repeat: matches 7454. .7774
                                                                                                                                                                                                                                                                                          /note="HERVK4 repeat: matches 1...1
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/note="L1 repeat: matches 4060. .4853 of con
L1 repeat: matches 4060. .4853 of consensus"
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LTR40a repeat: matches 2. .327 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                  LTR14A repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :e="MADE1 repeat: matches 34. .77 of consensus
:1 repeat: matches 34. .77 of consensus"
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95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from Ml3rev to -21Ml3 of the BAC clone. This sequence of OSJNBB0014K06 clone has an overlap with p0439E07 clone (DDBJ: AP003768) at the position 12.063 to 177.263 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA linear PLN 18-JUL-2002 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC clone:OSJNBa0014K08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468) on Jul 17, 2002 this sequence version replaced gi:20975425. On Jul 17, 2002 this sequence version replaced gi:20975425. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBU Non-Barandam Juries in Jarabase or
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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2 (bases 1 to 177263)
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3405. .3547,5098. .5199,6055. .6167,6605. .6690,7352.
/gene="OSJNBa0014K08.1"
complement(join(1396. .1701,1758. .2043,2410. .2544,
3405. .3547,5098. .5199,6055. .6167,6605. .6690,7352.
/gene="OSJNBa0014K08.1"
/translation="MAEPDWILERERRQVEQILELDMEELQVEEVDDAGSSSSEVDT FLRNTHBDGGGRTSEALAFNTSVVSLETCDGGVVLFEBAILPIRVVQPRSLTAVDKAV NHVDAPCMIGVIHHIKQLDGSSNVVTRGQNRFRLRRWIDADDVALISRRSDGPVGA YVKQTSCGQEMMTVYNATGLALRGAFSKAHSLEPGPTAIPQRRGFEKRCHHGGHDIQD AAIAHLKRCGFYLEKLAKKGRGNSPQRRGGAPRRLRVPTGNEEDDPPPLAPFALPLGR
                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:39947"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                /protein_id="BAC05577.1"
/db_xref="GI:21902028"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
http://www.sanger.ac.uk/HGP/Chrl
RP4-813B7 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on Jul 14, 2000 this sequence version replaced gi:8894204. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 127682)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATATATATCTACATTCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence is the entire insert of clone RP4-813B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                    AluY repeat: matches 239. .538
                                                                      complement(565
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                      /note="L1M4 repeat: matches
complement(565, .1283)
  'note="L1M4 repeat: matches 2732.
                                            note="match: GSS: Em:AQ383567"
                                                                                                                                   'note="L1M4 repeat: matches 2227.
                                                                                                                                                                             'note="L1M4 repeat: matches 2107.
                                                                                                                                                                                                                       /note="AluY repeat: matches 75. .310 of consensus
/luY repeat: matches 75. .310 of consensus"
                                                                                                                                                                                                                                                                                           clone_lib="RPCI-4"
                                                                                                                                                                                                                                                                                                                  /clone="RP4-813B7"
                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      .127682
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                                                                                                                                                                             .2438 of consensus'
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  .3226 of consensus
                                                                                      .3669
                                                                                                                                .2438 of consensus
                                                                                    0f
                                                                                    consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                     misc_feature
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                  /note="match: GSS: Em:AQ076436"
5154. .5605
                                                                                                                                                     5143.
                                                                                                                                                                 4636. .4942

/note="AluSc repeat: matches 1. .308 of con
AluSc repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (906.
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/note="match: GSS: Em:AQ896860"
                                                                                                                                                                                                                                                                                                      complement(3956
                                                                                                                                                                                                                                                                                                                                                                                                                3074. 3453
/note="match: GSS: Em:AQ261089"
3074. 3302
/note="match: GSS: Em:AQ059372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ009565" 3074. .3453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2626
                                                                                                                                                                                                                                                                                                                                                   complement(3620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /1999 .2404
/1999 .2404
/note="ILIM4 repeat: matches 3935. .4135 of consensus"
// repeat: matches 3935. .4135 of consensus"
// repeat: matches 3935. .4135 of consensus"
                                                                                                                                                                                                                                                                                                                                                                        3407. .3448
/note="MER5B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match: GSS: Em:AQ879547"
                                                                                                                                note="match:
                                                                                                                                                                                                                                          1136. .4803
/note="match: GSS: Em:AQ531595"
                                                                                                                                                                                                                                                                                      note="match: GSS:
                                                                                                                                                                                                                                                                                                                                  /note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1592. .2208

'note="LIMB1 repeat: matches 5338.

LIMB1 repeat: matches 5338. .5979 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1466. .1877
/note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS:
1451. .1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="match: GSS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="match: GSS: Em:AQ826107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="match: GSS: Em:AQ761517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2017
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                                                                                    GSS:
                                                                                                                                                                                                                                                                                                                              20. .4114)
GSS: Em:AQ117010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS: Em:AQ245895"
87. 3061)
GSS: Em:AQ608022'
                                                                                                                                GSS:
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                                                                                 Em: B60185'
                                                                                                                                Em: AQ224449"
                                                                                                                                                                                                                                                                                      Em: AQ304953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Em: AQ275646"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Em: AQ490007
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                                                                                                                                                                                                                                                                                                                                                                          .42 of consensus'
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(1572...1631.1701...1)
/gene="SPBP8B7.01c"
complement(join(1572...1631.1701...1)
/gene="SPBP8B7.01c"
/note="SPBP8B7.01c"
/note="SPBP8B7.01c, len:102"
/codon_start=1
/labe1=SPBP8B7.01c
/product."hypothetical protein"
/protein_id="CAA21786.1"
/db_xref="G1:3810825"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ctaacaacagcttag, spli
complement(1879...1884)
/gene="SCBP8B7.01c"
/note="gtacgt, splice donor s.
2917...3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SPBP8B7.02"
/note="SPBP8B7.02, len:261, SIMILARITY:Oxytricha fallax.
/note="SPBP8B7.02, len:261, SIMILARITY:Oxytricha fallax.
0 00905, hypothetical 129.9 kd protein., (1088 aa), fast
sco res: opt: 119, E():3.4e-05, (21.3% identity in 254
aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                SLLTFTRHDSEDVSTSVEKLTSKKISELEKLFADYCSIEDAFD"
complement(4027. .5118)
/gene="SPBP8B7.03c"
/gene="SPBP8B7.03c"
/note="SPBP8B7.03c, len:363"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1632. .1646)
/gene="SPBP8B7.01c"
/note="ctaacatagctgtag, splice
complement(1695. .1700)
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/translation="MAAARFTVSIYSKDGSVSSETIALPEVEKAPIRPDLVRSVHTAV
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APTKTWRKWHVKVNQNEKRYAISSAVAASGVFSLLLARHRRHVQRRGPLVVENEDAGIV
KAFRNIPGVEIVNVRLINLDLAPGGHLGREVIWTKSAFGLLDSVFGSTTEAAQLKKN
YFLPENIISNADVTRLINSDEIQSIVKAAGPSRVKRAHVQKKNPLKNKAVLARLNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="sptrembl:094252"
/translation="mndeeshisvlpymnkotslvlonlkeetenqlkelekkrsqlh
keqqinlqlyaindlrsktxelkaenekedtflnsfnasgdltankkiqlreqsrkl
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kdcrsliaeqllqsasllndfqndsdriaknhsslidtsrahrysltnatknythifd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SPBP8B7.02"
2917. .3702
                                                                                              complement(4330. .5064)
/gene="SPBP8B7.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein."
/protein_id="CAA21787.1"
/db_xref="GI:3810826"
join(5912. .5983,6026. .8413)
/gene="spBP8B7.04"
                                                                                                                                                                                                                                                                                                                               /product="60s ribosomal protein
/protein_id="CAA21788.1"
/db_xref="GI:3810827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="gtatgc, splice donor sequence"
complement(1837, .1852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {	t ATGMAIPHLVELSDKYKRQGYNISMDTATVEFMDEIVDEVSIQNKNRLGNVLLLRVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4896"
/chromosome="II"
                                                                                                                                           KAYKANVKLNTGKTPKAAGEKFLTVLHEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=SPBP8B7.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SPBP8B7.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SPBP8B7.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:094251"
/translation="MSVERIKRAPAFRKGIIIRRKTHLIAMIRRMRKKLDIDGSILYQ
                                                                     note="Pfam match to entry PF00573
                                                                                                                                                                                                                                                                                                                                                                                                          /label=SPBP8B7.03c
                                                 amily L1e"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  branch
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                                                                          Lle,
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                                                                        Ribosomal protein
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CLEARS INTO = "MINIANIKLYWNENDELIADMLLILKLSPRSSDCLLDLRDRKW
ELVOCKELNIGNERWPLNYDLFELPYNSLELDGSYSNUDFKHYVSONVELNHKTOVDF
TEQLIPKKSLNKLNGTLRETMSAMPSFES ISLONSVSNUDFKHYVSONVELNHKTOVDF
TEQLIPKKSLNKLNGTLRETMSAMPSFES ISLONSVSNUDFKHYVSONVELNHKTOVDF
TEQLIPKKSLNKLNGTLRETMSAMPSFES ISLONSVSNUDKSCHNDDWITIESEFSP
TEQLIPKKSLNKLNGTLRETMSAMPSFES ISLONGLSORAAATSTTPVCN
ISSVTSAINSVGEISNASHSSSTSELPCTYGNTSSIFQVKNEMSNIKSAISEGYIAHD
QOSKKVSVONIKKEFLIPFEFSLEGGFLNYNKFFSNLYKVLSEFEKTRDSKVMFTFRL
VLKTKPLYASESEFYETKLNFFTFPLECAINFHIDCSCFDDWRLFSLKESSSVAVPIP
KIKKESGRSWFQSLLFOFHHCLFPFLSWINYKOSQLNILTTETTIRPRICAAYQKLEY
NILVLLNEKPSSGSQLILSASPTCTIENIYIENTRLHPSKSQTPEQTVISFIDVQCVK
VTEARKTLELSYILSASPTCTIENIYIENTRLHFSKSQTPEGTVISFICHSKHEY
FLHFSSSYIFNDARERDVYGVKLSKNMWISMAYVDNCEANFFCKDLEYYDIYIKFKLLAD
WRLLTNPVLQIGEISDYCHFKLLKKVNMNISMAYVDNCEANFFCKDLFYFTTSRKQI
LLEIGILIKPERYNLFKYRYLLONFLPPTDSRTLVEROTIVTNSTLLFDGSFYFSQ
LLEIGILKPERYNLFKYRYLLONFLPPTDSRTLVEROTIVTNSTLLFDGSFYFSQ
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ELNGKDIDELIAAGNEKLATVFTGGAASAAPAAAAGGAAPAAEEAAKEEEEESDE
DMGFGLFD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry PF00484 Pro_CA, Prokaryotic-type carbonic anhydrases" complement(8937...9272)
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/translation="Medrikrrieeidhqdeiidreastaspvsgagkidqngeikdl-
/translation="Medrikrrieeidhqdeiidreastaspvsgagkidqngeikdl-
Lernultw8q079srkyesef*Taykd107pQvLwIgCsDsrvpffTilnillpgyvfvHrn
IANVVPRSDINALAVMEYSVTVLKVKHIIVCGHYGCGGVAAALGPNLNNLLDHWLRHI
RDVIEDNREELDAIEDPQLRRLKLAELNTRAQAISVTRVGFVREAMEKRGLQVHGWIY
DLSNGQIKKLDIDDAIKARKYGTYDS"
complement(8754__8822)
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/gene="SPBP8B7.05c"
/note="SPBP8B7.05c, len:244, SIMILARITY:Porphyridium
/note="SPBP8B7.05c, len:244, SIMILARITY:Porphyridium
purpureum., Q43060, carbonic anhydrase, (571 aa), fasta
scores: opt: 580, E():2.2e-31, (41.6% identity in 221 aa
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complement(8688..9422)
/gene="SPBP8B7.05c"
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6013. .6025
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CLLTLLIGIYLILQVVFIYTN"
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/protein_id="CAA21789."
/db_xref="GI:3810828"
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/protein_id="caA21790.1"
/db_xref="GI:3810829"
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join(10661. 10969,11033. .11056)
/gene="rp14-2"
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8B7.04#
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No. 2.6e+02;
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Homo sapiens chromosome 16 clone RP11-542M13, complete sequence.
ACO92723 ACO68615
                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US. On Feb 6, 2002 this sequence version replaced gi:15055296. Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-JUL-2001) Production Sequencing Facility, DOE Joenome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, Jases 1 to 188458)
DOE Joint Genome Institute.
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Sequencing of Human Chromosome
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Mammalia; Eutheria;
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                                                                                                                                                              Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
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                                                                            Base-by-base quality values are not generally visible from GenBank flat file format but are available as part of this entry's ASN.1 file.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome 1 was sequenced by the Sanger Centre. The sequencing of the S. pombe genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project.

Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program S3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the splice doncr/acceptor sites.

CDS are numbered using the following system eg SPBC25H2.01c. SP (S. pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $PBP8B7 71000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $75000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $750000 | $7500000 | $750000 | $7500000 | $7500000 | $7500000 | $7500000 | $7500000 | $7500000 | $7500000 | $75000000 | $750000000 | $75000000 | $7500000000 | $75000000 | $750000000000 | $750000000000000 | $75000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and Max Planck Institut fuer Molekulare Genetik, Ihnestr. 73,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.

1 (Dases 1 to 71000)

Beck,A., Reinhardt,R., Lyne,M., Rajandream,M.A. and Barrell,B.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe
Schizosaccharomyces pombe
                                                                                                                                                     (complementary strand).

(complementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The sequence MAY NOT be the entire insert of the sequence clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Pl pBB7 is overlapped at the 3' end by cosmid c19F5, EMBL entry SPBC19F5, accession number ALO22599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-14195 Berlin, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
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the world Wide Web.
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/organism="Schizosaccharomyces pombe'
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                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yeast sequencing at the Sanger Centre are available on
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, P., Telfrod, B., Thomas, N., Thomas, S., Usnani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watliamson, A., Wleczyk, R., Washington, C., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-JUL-2002) Human Genome Sequencing Center, Depois Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA on Jul 12, 2002 this sequence version replaced gi:18092762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Direct Submission
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                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Shemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 99284 bases at least Q40
Consensus quality: 104691 bases at least Q30
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murldae; Murlnae;
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH330-118H3"
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HTG 13-JUL-2002 G IN PROGRESS

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Sequencing vector: plasmid; 72%

Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319

Consensus quality: 206799 bases at least Q40
Consensus quality: 207057 bases at least Q30
Consensus quality: 207288 bases at least Q30
Consensus quality: 207288 bases at least Q20
Insert size: 217000; agarose-fp
Ouality coverage: 10.57 in Q20 bases; sum-of-contigs
Quality coverage: 11.06 in Q20 bases; sum-of-contigs
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22; Conserv
l (bases 1 to 83661)

1 (bases 1 to 83661)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Alsbrooks,S.L., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                             AC123500.2 GI:21909244
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-118H3, *** SEQUENCING
***, 41 unordered pieces.
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                                                                                                                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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2455. .207614
/note="assembly_name:Contig27
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1177. .2354
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/db_xref="taxon:9606"
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/clone="RP11-1296011"
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Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 83661)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-JUL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 19, 2002 this sequence version replaced gi:21240448.
* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is
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8162. .8500
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2549. .2861
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1628. .1825
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2. .12313
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}. .20967
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                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission Submitted (21-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA On Jan 3, 2002 this sequence version replaced gi:17027321.
                                                                                                                                                                                                                                                                                                                   207614 bp DNA linear HTG 03-JAN-2002 HOME SEQUENCE, 3 unordered pieces.
Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 207614) Waterston, R. H. The sequence of Homo sapiens clone
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23972. .24318
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29038. .29062
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28812. .29038
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23425. .23530
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29082. .29313
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Eukaryotta; Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 175895)

Sulston, J. E. and Waterston, R.

Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
Kruchowski,S., Kozlowicz,A.,
The sequence of Homo sapiens
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                                                                                              (bases 1
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/translation="MPTEIREIRPQSISRYEEMMSPYFAGFLYIATVLTGLFGNIWVV
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CRAMFVLENGVKITSLTVLSCISIERYITIRRPFCSEVRRQFVNATPIGASIFYGLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="for a graphical representation of this gene see: http://www.wormbase.org/db/seg/sequence?name=T07F8.2;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSSTVPIMQFPTPHFAPPMLTPHHHMLKYVYLQQHQQAQTFLKGAAGLHPGTHIMFPP
PIIVDGSFGARYSSNIYPFSYIVPQNFNFLNGNFGHL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAITYQINSYTYSSDGLNCVERSYRGKAIPRVASYLTAVAFLVDLTIISLNYSGIYRHV
RRKFTKRRARVQANGRURESLIVNEPRYMTEMTAAIIVRVYTHVVCWLLPKLMQFIFDN
TIQSELTAGIRLFSNERDYSITRWLLIFIATWLTSMNAACDWIFYAVMNRDLRNLLSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEVPLNCASLRSKEFNIKKLYTAYQKVLSKKFDFIAPQPNDYDNSIWHHSLPANFLKN
FNMPCRGELSDGSNGRRHRSSSIASSRSKHSYMSKGKQFSESSGGPSRSHTRVSSFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYYVDQVLGSSSTAQLMPVIERETTTIISYPCYNNRNETRGNIYEIKVVGNIDNVLK
ARRYIMDLLPISMCFNIKNTDMAEPSRVSDRNIHMIIDESGIILKMTPSVYEPADLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>EMSFVDAPEKNGIVTTYLRITAREKNQHELIEAAKRLNEILFRESPAPENNFTLHFTL</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDPFAQQVTITGYFGDVDRARMLMRRNCHFTVFMALSKMKMPLHELQAHVRQNPIQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin heavy chain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=T07F8.1;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical protein T07F8.2"
/protein_id="AAB38097.1"
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17739. .17866,18090. .18163,18212. .18319,20099. .20139,
00265. .20325,20372. .20426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="T07F8.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="weak similarity in 5' end of exon 1 to C. elegans myosin heavy chain B; 3' end of exon 1 similar to ZK686.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="T07F8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKFIYFQSSAIGEKKISSSRAGSSNIKNPLQRTIFFCFIPNFSQSTRKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exons 2 and 4 similar to transmembrane and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="T07F8.
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                                                                                            to 175895)
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95.7%;
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Pred. No. 1.
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                                            Hawkins, M., Elliot, G. BAC clone RP11-368M16
                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  somatostatin receptor type 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                             linear
complete
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                                                                     Doebber, A.
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                                                                                                                                       Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Aug 9, 2001 this sequence version replaced gi:14589722.
                                                                                                                                                                                                                                               Waterston, R.
                                                                                                                                                                                                                                                                                                                 Submitted (09-AUG-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                        4 (bases 1 to 175895) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                 MO 63108,
                                                                                                                                                                                                                                                                           (bases 1 to 175895)
Center project name: H_NH0368M16
                                             Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                      63108,
                                                                                                                                                                                                                                                                                                                        Louis
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clone sections once, between neighboring data submissions This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping ections once, or longer because we provide a small overlap

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 17 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nh.gov/DR/GTB/CHRI7. seed http://www.nhgri.nh.gov/DR/GTB/CHRI7. mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

В δõ

VECTOR: PBACE3 6
VECTOR: PBACE3 6
NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-368M16;
Actual start of this clone is at base position 175895 of RP11-368M16. The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

source 80620 CO 80630 Location/Qualifiers 51174 to 51278 and

FEATURES

/clone="RP11-368M16" /clone\_lib="RPCI-11" /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="17"

CDS

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                                                              source
                                                                                                     Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORPecome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
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500 bp
of T071
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Submitted (04-DEC-1996)
4 (bases 1 to 23862)
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http://www.wormbase.org/db/seq/sequence?name=T07F8;class=Sequence
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Louis, MO 63110, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         more than one m13 subclone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pauley, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T07F8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmid is F10E7, 1000 bp overlap; the 3' cosmid is C27H5 overlap. Actual start of this cosmid is at base position F8; actual end is at 12559 of C27H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Genetics, Washington University St. Louis , MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Эď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Sequencing Center
Department of Genetics, Washington
St. Louis , MO 63110, USA, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence may not be the entire insert of this clone shorter because we only sequence overlapping sections longer because we provide a small overlap between
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (5396),
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FVSSALKDIIVNEFESOYVSLMYSDNGDHENDAMEDRHYDAHDHVRONPIONV
ENFAQOVTITGYFGDVDRARMLMRNCHFTVFMALSKMKMPLHELOAHVRONPIONV
MSFPOQOVTITGYFGDVDRARMLMRNCHFTVFMALSKMKMPLHELOAHVRONPIONV
EMSFVDQDYLGSSSTAQLMAVIERETTIISYPCYMNRNEFERNIYEIKVVGNIDNVLK
STYVDQVLGSSSTAQLMAVIERETTIISYPCYMNRNEFERNIYEIKVGNIDNVLK
ARRYINDLLPISMCFNIKNTDMAEPSRYSDRNIHMIIDESGIILKMFPPSYYEPADLLS
GEVPLNCASLRSKEFNIKNTDMAEPSRYSDRNIHMIIDESGIILKMFSPANFLKN
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VERGYFROHQRLOKDDQORWKTGSRGDHSKRTINVHRDVRNSNEYDFHYGARR
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VERGYFROHQRLOKDDQORWKTGSRGDHSKRTINVHRDVRNSNEYDFHYGARR
VERGYFROHQRLOKDDQORWKTGSRGDHSKRTINVHRDVRNSNEYDFHYGARR
VERGYFROHQRLOKDDQORWKTGSRGDHSKRTINVHRDVRNSNEYDFHYGARR
VERGYFROHQRLOKDDORWKTGSRGDHSKRTINVHRDVRNSNEYDFHYGARR
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5179. .5344.5389. .5515,5560. .5681,5728. .5805,5850.
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                                                                                                                             /note="coded for by the following C. elegans cDNAs: yk345b5.3, yk719f7.3, yk345b5.5, yk719f7.5" codon_start=1./product="Hypothetical protein T07F8.3b" /protein_id="AAK77630.1" /db_xref="GI:15011799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPSLEQVQLQMTHHLKLKSNDVDLDHEKLYMHESPHNDSDTTVSASGFGNDLMDGDFV
QRFLSNANINESGRRPRTVSCFTEKDGQSARYIDSDGAYSVVDHASTHQSRSYDSFRK
VGDNGVTKTILEPRARVEKDYGKISLEHKTKYSNEYGDEEKSAENDTSSLGSRQYRID
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5179. 5344,5389. 5515,5560. 5681,5728. 5805,5850.
6035. 6277,6326. 6424,6473. 6641,6784. 6906,6951.
7355. 7432,7477. 7716,7764. 8190,8310. 8591,8820.
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/db.xref=01:1708761"
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MGNUSGGTDDDDDDXAFPDDFWKRSIRVDFVLFQADVPLFNBATVEESSAAAEPHDSTIFD
MGNUSGGTDDDDDDXAFPDDFWKRSIRVDFVLFQADVPLFNBATVEESSAEREDDTIKAR
IDQTNQPSDEVIDNYLKDVVGLRKAHDQPCPPAGTESRDDEDALCALYRSNFDTEKAR
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/translation="MGEQSHEKDHDEAHSYNPFVRSAVEYDADTRLQMAENAASARKL
FVSSALKDIIVNPENFYHDFQQSAQMAEDANQRRQVSYNTKREAHIHQLKAQGLPLPS
NIPMIEINPTRVTLNMEFESQYYSLMTSDNGDHENVASIMAETNTLIQLPDRSVGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMKRNIYILRNRDESNSFEYFLHQFSLYMNPICAYRIRLHQFLSYKPSICLSRISLYP
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/note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=T07F8.3a;clas
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3401..3596,3646..3755,3798..3854,3906..3987))
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EYYYQWKLTPGYRVWRDAHPQHAPVVQPHLSAAWHQQVAQLEDQNGQTGFVEASFSEP
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/gene="T07F8.4"
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/note="coded for
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2000000000
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Perfect score:
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25
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    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1 U80954 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE		4.4 4.5	4-4	4.4	C 40	ıω	c 37	ນເພ	0 34	(	. w c	30.0	22 5	C 26	S NO	C 23	, N	c 21	c 19	<u>ب</u> بر	C 15	i iii	13	c 12	10	0		10	· .	<i>س</i> ح	21	• (1	
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Sequence 29, Application US/09873880

Ratent NO. US20020123118A1

GENERAL INFORMATION:

APPLICANT: Sewalt Vincent
APPLICANT: Sewalt Vincent
APPLICANT: Falco, S. Carl

APPLICANT: Alico, S. Carl

APPLICANT: Alico, S. Carl

APPLICANT: Alico, S. Caphen M.

TITLE OF INVENTION: GLYCINE METABOLISM ENZYMES
FILE REFERENCE: BB1192 US CIP
CURRENT FILLING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/363,321
PRIOR IFILING DATE: July 28, 199
PRIOR APPLICATION NUMBER: 60/094,839
PRIOR FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Microsoft Office 97
SEQ ID NO 29
LENGTE: 1362
TYPE: DNA
ORGANISM: Glycine max
US-09-873-880-29
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US-09-873-880-29/c
Search completed: July 8, 2003, 06:04:29 Job time : 25.6338 secs
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715 AGCGGATTTGTAGATTGTG 733
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FEATURE:

NAME/KEY: UNSUTE

LOCATION: (382)

OTHER INFORMATION: n=A, C,

NAME/KEY: UNSUTE

LOCATION: (454)

OTHER INFORMATION: n=A, C,

US-09-873-880-7
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US-10-172-086-11
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                                                                                                                                                                                                                                                                                                             SOFIWALL SEQ ID NO 7
                               Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local S
Matches 18
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CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 11
LENGTH: 5310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sewalt, Vincent
APPLICANT: Falco, S. Carl
APPLICANT: Alien, Stephen M.
TITLE OF INVENTION: GLYCINE METABOLISM ENZYMES
FILE REFERENCE: BB1192 US CIP
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/873,880 CURRENT FILING DATE: 2001-06-04 PRIOR APPLICATION NUMBER: 09/363,321 PRIOR FILING DATE: July 28, 1999 PRIOR APPLICATION NUMBER: 60/094,839 PRIOR FILING DATE: July 31, 1998
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 42
SOFTWARE: microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method and nucleic acids for the differentiation
TITLE OF INVENTION: of prostate tumors
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                             LENGTH: 495
TYPE: DNA
ORGANISM: Glycine max
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Pred. No. 3.2e+02;
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                                       US-09-738-626-2066
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US-09-738-626-2066
                                                                                                                                                 APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKTO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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LENGTH: 920
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                SOFTWARE: PatentIn ver. 3.0 SEQ ID NO 2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/10001879 Patent No. US20020127237A1
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APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes
FILE REFERENCE: DEX-0.881
CURRENT APPLICATION NUMBER: US/10/001,879
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION UNMBER: 60/252,188
PRIOR APPLICATION UNMBER: 60/252,188
PRIOR FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 201
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Salceda,
                                               TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                               LENGTH: 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692 GGGGATGAGGAGATTGTGA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 AGGGGATTTGGAGGTTGCG 335
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIROSHI
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Score 15
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Pred. No. 4
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DB
9;
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOSTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 34536
LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 422
TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-757-417-23
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CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 23
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SEQ ID NO 33366
LENGTH: 430
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
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Publication No. US20030073623A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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TYPE: DNA
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Local Similarity 85.7%;
les 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foy, Theresa M
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Pred. No. 2
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Pred. No. 2
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RESULT 10
US-10-172-086-42
US-10-172-086-42
; Sequence 42, Application US/10172086
; Publication No. US20030113750A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; APPLICANT: Epigenomics AG
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US-09-938-842A-4643/c
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APPLICANT: Wang, Xun
APPLICATION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIF1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILLING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILLING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-172-086-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4643
LENGTH: 2000
                                                                                                                     TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: Of prostate tumors
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 42
SEQ ID NO 42
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Best Local Similarity 85.3
Matches 18; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(475)
OTHER INFORMATION: n = A,T,C
                                      TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                       LENGTH: 5118
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85.7%;
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85.7%;
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Pred. No. 2
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Pred. No. 2.
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Query Match

Score 16.2;

DB

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RESULT 4
US-10-102-524-97
; Sequence 97, Application US/10102524
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US-09-815-242-7388
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PPLICATION NUMBER: 60/296,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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NUMBER OF SEQ ID NOS: 43
SEQ ID NO 11
LENGTH: 21000
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                        Query Match
Best Local
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7388
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                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (1).
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/2 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Helicobacter
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                                                                                                                                                                     Local Similarity
nes 17; Conserv
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1787 AGGGGATTTGGACCTTGTGA 1768
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Trawick, John D.
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Pred. No. 1
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1.9e+02;
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APPLICANT: Fling, Steven P.
APPLICANT: Foling, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Wang, Ajjun
APPLICANT: Wang, Ajjun
APPLICANT: Wonsil, Patricia D.
APPLICANT: Sutherland, R. Alec
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY,
TITLE OF INVENTION: DIAGNOSIS AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.479C3
CURRENT APPLICATION NUMBER: US/10/042,945
CURRENT FILING DATE: 2002-01-08
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 422
TYPE: DNA
CREATER AND ANTESSED ID NO
                                                                         RESULT 6
US-09-757-417-23/c
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                                                                                                                                                                                                                                                                                                     ORGANISM: Oryctolagus cuniculus US-10-042-945-23
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US-10-042-945-23/c
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SEQ ID NO 97
LENGTH: 186
GENERAL INFORMATION: APPLICANT: Fanger,
                                   Sequence 23, Application US/09757417 Patent No. US20020082216A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/10042945 Publication No. US20030045468A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEO ID NOS: 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 15, 51
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Pred. No. 2.2e+02;
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Pred. No. 2
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Minimum
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Listing first 45 summaries
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Perfect score:
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length: 2000000000
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  l: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2 /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3 /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3 /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5 /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5 /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7 /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8 /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9 /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10 /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
11 /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12 /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
13 /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
14 /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
15 /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
16 /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17 /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18 /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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10 US-09-873-880-7
11-001-879-38
10S-09-738-626-2066
10 US-09-873-880-29
10 US-09-873-821-17
10 US-09-778-623-17
10 US-09-770-445-539
10 US-09-991-630-23
                                                                                                  US-09-918-995-33366

US-09-918-995-34536

US-09-938-842A-4643

US-10-172-086-42

US-10-172-086-11
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US-09-815-242-7388

US-10-102-524-97

US-10-042-945-23

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Sequence 11, Appl
Sequence 7388, Ap
Sequence 27, Appl
Sequence 23, Appl
Sequence 3356, A
Sequence 34536, A
Sequence 4643, Ap
Sequence 11, Appl
Sequence 7, Appl
Sequence 206, Appl
Sequence 207, Appl
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Sequence 80, Appl Sequence 29, Appl	212	Sequence 2192/, A	Sequence 9, Appli		Sequence 2254, Ap	53	e 46	Seguence 46, Appl	Sequence 5415, Ap	e 144	Sequence 2921, Ap	e 253	ce 1079	Sequence 1382, Ap	Sequence 1382, Ap	Sequence 1382, Ap	Sequence 1382, Ap	Sequence 2706, Ap	on	122,	96,	7906,	

## ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Ta Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION UNBER: 09/333,535

PRIOR FILING DATE: 199-06-14

NUMBER OF SEQ ID NOS: 15775
                   RESULT 2
US-09-975-123-11/c
US-09-975-123-11/c
Sequence 11, Application US/09975123
Publication No. US20030087857A1
GENERAL INFORMATION:
APPLICANT: SUSAN M. Freier
APPLICANT: SUSAN M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR BINDING PRO
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0253
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: Sequence 4901, Application US/09878574

: Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-054-Q1-B1-B3
US-09-878-574-4901
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TYPE: DNA
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Best Local S
Matches 19
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Local Similarity 90.5%;
les 19; Conservative
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  APPLICATION
                                                                                                                                                                                                                                                                                                   TAGGGGATTTGGAGATTGTGA 21
NUMBER: US/09/975,123
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Pred. No. 43;
0; Mismatches
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Job time : 18.0371 secs

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RESULT 14
US-09-173-891-5/c
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                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENGTH: 3771 base pairs
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NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                            KEGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCU104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
CLONE: E. coli NM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                   FEATURE:
                                                                                                                        ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                        MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2421 N.W. CITY: Gainesville
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ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/173,891
NAME/KEY:
                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                               STRANDEDNESS: double
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                                                                                                     ORGANISM:
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                                                                                                                                                                                                                                nucleic acid
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2421 N.W. 41st Street, Suite A-1
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Schnepf, H. Ernest
Schwab, George E.
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Uick, Heidi Jane
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Randall, John Brow
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                                                                                                                                                                                              linear
misc_feature
4..24
                                                                                      Bacillus thuringiensis ISOLATE: 33F2
                                                  coli NM522(pMYC2316) B-18785
                                                                                                                                                                           DNA (genomic)
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US-09-076-137-5/c
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                                                                                                                                           US-09-076-137-5
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 5
LENGTH: 3771
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schwab, George
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. 6166195el Nematode-Active Toxins TITLE OF INVENTION: Therefor FILE REFERENCE: MA-20CCCD2
                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(24)
OTHER INFORMATION: /function- "oligonucleotide hybridization probe"
OTHER INFORMATION: /product= "GCA/T TTA AAT GAA GTA/T TAT"
OTHER INFORMATION: /standard_name= "probe a" /note= "probe A"
                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: (13)..(33)

OTHER INFORMATION: /function= "oligonuclectide hybridization probe"
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OTHER INFORMATION: /standard_name= "Probe B" /label= probe-b /note-
OTHER INFORMATION: "probe b"
                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis
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LOCATION:
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mes 17; Conserv
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1078 TAGGCGATTTGTAGAATGTG 1059
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                                                                   l Similarity
17; Conserv
                                 TAGGGGATTTGGAGATTGTG 20
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hybridization probe"
product= "AAT GAA GTA/T TAT CCA/T GTA/T AAT"
/standard_name= "Probe B"
/label= probe b
/note= "probe b"
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Pred. No. 2.
                                                                                      Score 15.2;
Pred. No. 2
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Search

completed: July

2003, 05:56:57

DATE:

12-AUG-1987

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RESULT 13
US-08-611-928-5/c
US-08-611-928-5/c
; Sequence 5, Application US/08611928
; Patent No. 5824792
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Kannedy. M. Keith
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Matches 17; Conserv
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INFORMATION FOR SEQ ID NO: 5 (PS33F2):
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                   APPLICANT:
APPLICANT:
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OTHER INFORMATION:
OTHER INFORMATION:
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/8

FILING DATE: 31-JAN-1992
             TITLE OF INVENTION: NO. 5824792el Bacillus thu:
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 13..33
OTHER INFORMATION: /func OTHER INFORMATION: /pto1
OTHER INFORMATION: /pto0
OTHER INFORMATION: /stan
OTHER INFORMATION: /labe
OTHER INFORMATION: /note
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                                                                 APPLICANT:
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CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
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                                                                              Meier, Henry
Uick, Heidi Jane
Foncerrada, Luis
Schnepf, H. Ernest
Schwab, George E.
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Kennedy, M. Keith
Randall, John Brooks
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                                                                 Jenny
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85.0%;
                                              No. 5824792el Bacillus thuringiensis Toxins Active
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hybridization probe"
/product= AAT GAA GTA/T TAT CCA/T GTA/T AAT"
/standard_name= Probe B"
/label= probe b"
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hybridization probe"
/product= GCA/T RCA/T TTA AAT GAA GTA/T TAT"
/standard_name= probe a"
/note= Probe A"
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2316) в-18785
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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US-08-611-928-5
Query Match
Best Local Similarity
Matches 17; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: dou
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,232
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
                                                                                                                                                      NAME/KEY: misc_feature LOCATION: 13:.33
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LOCATION: 4.24
OTHER INFORMATION: /func
OTHER INFORMATION: /bbri
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OTHER INFORMATION: /note
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LENGTH: 3771 base pairs
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CTTY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/611,928 FILING DATE: 06-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
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                        72.4%;
85.0%;
                                                                                               /function= "oligonucleotide hybridization probe"
/product= "AAT GAA GTA/T TAT CCA/T GTA/T /
/standard_name= "Probe B"
/label= probe-b
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                    Score 15.2; DB 1;
Pred. No. 2.2e+02;
      Mismatches
                                      Length 3771;
      Indels
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US-08-304-626-5/c
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Best Local Similarity
Matches 17; Conserv
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INFORMATION FOR SEQ ID NO: 5:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schnepf, Harry E.
APPLICANT: Schwab, George E.
TITLE OF INVENTION: No. 5616495el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Hymenopteran Pests and Genes Encoding
TITLE OF INVENTION: Hymenopteran-Active Toxins
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SECTION OF S
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: |
FILING DATE:
                                                                                                              ANTI-SENSE:
                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 32606
ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 33F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1078 TAGGCGATTTGTAGAATGTG 1059
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                                                                        SOURCE:
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Uick, Heidi Jane
Foncerrada, Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: David R. Saliwanchik
2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Randall, John Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Payne, Jewel M.
                                                                                                                                                                                      DNA (genomic)
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/product= "AAT GAA GTA/T TAT CCA/T GTA/T AAT"
/standard_name= "Probe B"
/label= probe-b
/note= "probe b"
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Pred. No. 2.2e+02;
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US-08-316-301A-5/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                          APPLICATION NUMBER: US/08/
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/871
FILING DATE: 23-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE: CLONE: E. coli NM522(pMYC2316) B-18785
                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 5753492el Nemator TITLE OF INVENTION: Which Code Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Payne, Jewel M. APPLICANT: Narva, Kenneth E. APPLICANT: Foncerrada, Luis
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                             FILING DATE: 03-MAY-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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LOCATION:
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nes 17; Conserv
                                              APPLICATION NUMBER: 07/5. FILING DATE: 10-AUG-1990
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                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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R INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                          UMBER: 07/693,018
03-MAY-1991
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85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function= "oligonucleotide hybridization probe" hybridization probe" hyproduct= "AAT GAA GTA/T TAT CCA/T GTA/T AAT" /standard_name= "Probe B" /label= probe b" hote= "probe b"
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                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
                                                                                                                                                                                             07/871,510
                                                              07/565,544
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Pred. No. 2
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APPLICANT: Narva, Kenneth
APPLICANT: Schwab, George
APPLICANT: Payne, Jewel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1 (PS33F2):
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 33f2 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: L10Yd, Jeff
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeff Lloyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FITLE OF INVENTION:
                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                  LOCATION: 13..33
OTHER INFORMATION:
OTHER INFORMATION:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 199304 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 4..24
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1078 TAGGCGATTTGTAGAATGTG 1059
                                                               l Similarity
17; Conser
                              1 TAGGGGATTTGGAGATTGTG 20
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                                                               Conservative
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                                                                                                                                                                                                                                                              misc_feature
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George E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Encoding No. 5439881el Nematode-Active Toxins Cloned from Bacillus thuringiensis Isolates
                                                                               72.48;
                                                                                                                                                                                                                                                                                                /function= "oligonucleotide hybridization probe" 
/product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT" 
/standard_name= "probe a" 
/note= "Probe A"
                                                                                                                                                                                hybridization probe"
/product= "AAT GAA GTA/T TAT CCA/T GTA/T AAT'
/Standard_name= "Probe B"
                                                                                                                                                 /label= probe-b
/note= "probe b"
                                                                                                                                                                                                                                /function= "oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/049,783
                                                            Score 15.2; In Pred. No. 2.2e 0; Mismatches
                                                               0;
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                                                             .2e+02;
les 3;
                                                                                                 DB 1;
                                                                                             Length 3771;
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Sequence 5, Patent No. !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
ANALY: CALLING DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
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                                 FEATURE:

NAME/KEY: misc_feature

LOCATION: 4..24

OTHER INFORMATION: /func

OTHER INFORMATION: /bybri

OTHER INFORMATION: /prod

OTHER INFORMATION: /stan

OTHER INFORMATION: /note
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                           IMMEDIATE SOURCE: CLONE: E. coli NM522(pMYC2316) B-18785
                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                              HYPOTHETICAL: | ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 5596071el Bacillus thuringiensis Toxins Active
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/
                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 33F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                          H: 3771 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
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Schnepf, H. Ernest
Schwab, George E.
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Uick, Heidi Jane
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Kennedy, M. Keith
misc_feature
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                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                           double
                                   /function= "oligonucleotide
hybridization probe"
/product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
/standard_name= "probe a"
/note= "Probe A"
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; LOCATION: (98)..(496)
US-09-262-773-5
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US-09-262-773-5
US-07-17 8
US-07-1876-280-5/c
; Sequence 5, Application US/07876280
; Patent No. 5262158
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US-09-262-773-1
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APPLICANT: Ballinger, Dennis G.
APPLICANT: Dennis G.
APPLICANT: Dennis G.
APPLICANT: Wagner, Susanne
APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: SUSCEPTIBILITY GENE CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 3268
TYPE: DNA
                                                                                                                                                                                   Query Match
Best Local S
Matches 17
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APPLICANT: Ballinger, Dennis G.
APPLICANT: Ding, Wei
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Best Local Similarity
Matches 17; Conserv
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LENGTH: 3264
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wagner, Susanne
APPLICANT: Hess, Mark A.
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORG
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
TILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT APPLICATION NUMBER: 1999-03-04
NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (98)..(2041)
                                                                                                                                                                                                                                                                                                                                   ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2993 AGGGGATTTGGAAACTGTCA 3012
                                                                                                               2997 AGGGGATTTGGAAACTGTCA 3016
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17; Conserv
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85.0%;
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Pred. No. 2.2e+02;
0; Mismatches 3;
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Pred. No. 2.2e+02;
0; Mismatches 3
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ches 3;
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TELEPHONE: 904-375-8100
TELEPAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3771 base pairs
TYPE: NUCLEIC ACID
                                                                                Query Match
Best Local :
                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: line
MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis INDIVIDUAL ISOLATE: 33f2
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRAJION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262158el
TITLE OF INVENTION: Controlling Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                               OTHER INFORMATION:
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ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                      NAME/KEY:
1078 TAGGCGATTTGTAGAATGTG 1059
                                                              similarity 85.0
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                              TAGGGGATTTGGAGATTGTG
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2421 N.W. 41st Street, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                       misc_feature
13..33
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                                                                               72.4%;
                                                                                                                                                                                 /function= "oligonucleotide
hybridization probe"
/product= "AAT GAA GTA/T TAT CCA/T GTA/T AAT"
/standard_name= "Probe B"
                                                                                                                                                                                                                                                                                                    hybridization probe"
/product= "GCA/T ACA/T TTA AAT GAA GTA/T TAT"
/standard_name= "probe a"
/note= "Probe A"
                                                                                                                                                 /label= probe-b
/note= "probe b"
                                                                                                                                                                                                                                                                                                                                                                         /function= "oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/07/876,280
                                                              Score 15.2; DB 1;
Pred. No. 2.2e+02;
0; Mismatches 3
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                                                                                                  DB 1;
                                                                                                  Length 3771;
                                                                  Indels
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; TYPE: DNA; Homo sapien US-09-404-879A-46
                                                                          ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-993-228-20
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US-08-993-228-20
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SEQ ID NO 46
LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5976838 GENERAL INFORMATION:
 Query Match 72.4%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20,
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Best Local :
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46202
FULL REFERENCE: 210121.46202
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILLING DATE: 1999-09-24
CURRENT FILLING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAS: (617) 876-5851
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF ENVIRONMENT OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/993,228 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jacobs, Kenneth APPLICANT: McCoy, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 87 Cambridge
                                                                                                                          LENGTH: 3113 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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R p1
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17; Conserv
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LaVallie, Edward R.
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                                                                                                                 linear
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Pred. No. 1.8e+02;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ballinger, Wei
APPLICANT: Hess, Mark A.
APPLICANT: Hess, Mark A.
TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Wagner, Susanne
APPLICANT: Hass, Mark A.

TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE
TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myriad 3
CURRENT APPLICATION NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
SOOTWARE: Patentin Ver. 2.0
SEQ ID NO 3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09262773 Patent No. 6225451
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TYPE: DNA
ORGANISM: human
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TYPE: DNA
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Pred. No. 2.2e+02;
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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; LOCATION: (127009)...(127130)
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; Sequence 46, Application U
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; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jenn
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     King, Gordon
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Length 168575;

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Sequence 1, Application US/09425290
Patent No. 6410712
GENERAL INFORMATION:
APPLICANT: BEGGING Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 168575
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US-09-605-785-507

US-09-439-313-508

US-09-439-313-507

US-09-149-476-224

US-09-149-476-224

US-08-70-651-4

US-08-70-651-4

US-08-983-502-14

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BASE COUNT
ORIGIN
Search completed: July 8, 2003, 05:51:38 Job time: 174.34 secs
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Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                          82.9%; Score 17.4; DB 12; Length 546;
94.7%; Pred. No. 1.4e+03;
tive 0; Mismatches 1; Indels 0
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1 (bases 1 to 488)

van der Hoeven,R., Bezzerides,J., Bachem,C., Horvath,B., Visser,R., Holt,I.E., Liang,F., Hansen,T.S., Utterback,T., Bowman,C.L., Doan,B., Bougri,O., Buell,C.R., Ronning,C.M., Tanksley,S.D. and Baker
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EST
1 (bases 1 to 535)
Buell, C.R., Hart, A., Baker,
Restrepo, S., Griffiths, H.,
                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Contact: Research Genetics,
Tel: 1-800-711-6195
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EST604136 mixed potato
5' end, mRNA sequence.
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                                                                                                                                                                                                            mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBlueScript SK(-): Site_1: EcoR1; Site_2: Xhol; RNA was supplied by Christian Bachem & Beatrix Horvath(Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the introduction of tuber formation as described in Bachem eal. (Plant Journal 1996). Tissue samples were taken of stages corresponding to growing stolons and the early stages of tuber formation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="potato stolon, C
/tissue_type="axillary buds
stolons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="1 to 3 days"
/lab_host="SOLR"
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/clone="cSTA30H15"
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/cultivar="Bintje"
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  Baker,B., Tanksley,S., Fry,W., Suhs,H., van der Hoeven,R., Tsai,J.
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Pred. No. 1.3e+03;
                                                                                                                                                                                                                              535 bp mRNA linear EST 22-JUL-2002 tissues Solanum tuberosum cDNA clone STMEB75
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Cornell University Solanum tuberosum
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BG147712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
                                                                                                                                                                                                                                                               Unpublished (1997)
Other_ESTs: mab53d02.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG147712 546 bp mRNA linear EST 01-FEB-2 mab53d02.x1 Soares_NMEBA_branchial_arch Mus musculus cDNA clone IMAGE:3974043 3' similar to TR:Q9VII5 Q9VII5 CG10286 PROTEIN. ;,
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18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, Email: potato@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
On Apr 17, 2002 this sequence version replaced gi:20170522
Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BG147712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cdna@resgen.com
Seq primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Possible reversed clone: similarity on wrong strand possible reversed clone: polyT not found High quality sequence stop: 488.

Location/Qualifiers
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                                                                                   MGI:1474075
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                                                                                                                     image.llnl.gov/image/html/iresources.shtml
                                                                                                                                          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information through the I.M.A.G.E. Consortium/LLNL at:
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/lab_host="SOLR"
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/db_xref="taxon:4113"
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1. .535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="STMEB75"
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L.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, I.I.n, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ell. Lin, H., van Damme, M., Lavelle, D., Livingston, K., Zhou, Y., Lai, Z., P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z. Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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EST.
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BQ859778 BQ859778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig1855, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Alexander Kozik [R.W.Michelmore]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGC13 row: P column: 11.
                                                                                                                                                /note-"Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5 and 3 tags to distinguish each source of RNA, cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB-QG_EFGHJ lettuce serriola TAG_TISSUE-germinating seeds
TAG_TISSUE-TCTGTGCGGG"
                                             TAG_SEQ=TGTAGCCGGG"
                                                                       construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=QG_ABCDI lettuce salinas
TAG_TISSUE=chemical induction
                                                                                                                                                                                                                                                                                                                                                                   /organism="Lactuca sativa"
cultivar="salinas"
/db_xref="taxon:4236"
/clone="0cC13P11"
/clone_lib="QG_ABCDI lettuce salinas"
/lab_host="E.coli"
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90.5%;
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Pred. No. 9.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://cgpdb.ucdavis.edu/
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56 TIGGCGATITGGAGATIGTGA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Alexander Kozik [R.W.Michelmore] bepartment of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1 (530) 742-1742 Fax: 1 (530) 752-9659
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Rozik, M., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellis, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project
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                                            1 TAGGGGATTTGGAGATTGTGA 21
                                                                                         l Similarity
19; Conser
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Plate: QGG5 row: L column: 02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://compgenomics.ucdavis.edu/
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                    /note="Vector: pBrcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size blas. Details of each source of RNA and library
                                                                                                                                                                                               construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_TISSUB=germinating seeds
TAG_SEQ=TCTGTGCGGG°
170 c 175 g 218 t
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/clone="QGG5L02"
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/cultivar="L.serriola"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E.coli"
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90.5%;
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Pred. No. 9.7e+02;
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                                                                                       Mismatches
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Best Local :
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QGG1C03, yg.abl QG_EFGHJ l
QGG1C03, mRNA sequence.
B0998627
B0998627.1 GI:22433023
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                                                                                                                                                                                                                                                                                                                                  Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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DNA is from a doubled haploid
Seq primer: TR
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Town, C.D., Van Aken, S.,
                                                                                                                                                                          Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
Driversity of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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                                                                                                                                       Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig1855, see http://cgpdb.uc
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Unpublished (2002)
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/note="Vector: pHOS1; Site_1: BstXI; 2
genomic DNA inserted into pHOS1 using
a 159 c 139 g 179 t
/organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
                                                                Location/Qualifiers
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/clone="BOGGB88"
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/strain="TO1000DH3"
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}.5e+02;
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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BQ997349.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig1855, see http://cgpdb.uc
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//Llob_host="E.Coli"
//Lab_host="E.Coli"
//note="vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=GQ_EFGHJ lettuce serriola
TAG_SEQ=CGAATGGGGG"
211 t
/note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5′ and 3′ tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and
                                                                                                                                                                                                                 /cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGG16D11"
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                                                                                                                                                               /clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
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Pred. No. 9.6e+02
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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19; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Grops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://compgenomics.ucdavis.edu/
Unpublished (2002)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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EST.
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BU002845
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QGG33D01.yg.abl QG_EFGHJ
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1-(530)-752-9659
                                                                                                                                                                                                                                                                      /note="Yector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=QC_EFGHJ lettuce serriola
TAG_TISSUE-germinating seeds
TAG_SEQ=TCTGTGCGGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="QG_EFGHJ lettuce serriola"
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Pred. No. 9.3e+02
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
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BOGGB88TR
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Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                               sequence.
BH541998
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Fax: 1-(530)-752-9659
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BQ996610.1 GI:22431006
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/clone="QGG13F01"
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/lab_host="E.coli"
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                                                                                                                                     GI:17793048
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90.5%;
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Pred. No. 9.
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Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library Unpublished (2001)
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HVSMEn0016I16f Hordeum vulgare rachis EST library HVcDNA0015
(normal) Hordeum vulgare cDNA clone HVSMEn0016I16f, mRNA sequence.
B1958770
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rar
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Clemson University
- Ann Hall, Clemson,
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864 656 4293
1: rwing@clemson.edu
                                                                                                                                                                                                                                                                     /note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2: /note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the racchises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                    see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
a 172 c 175 g 187 t 26 others
                                                                                                                                                                                        sequence analysis see http://www.genome.clemson.edu/projects/barley. To order
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1. ..715
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/lab_host="TJC121"
                                                                                                                                                                   this clone see http://www.genome.clemson.edu/orders Also
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/clone="HVSMEn0016I16f"
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/cultivar="Morex"
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85.7%;

Score

18;

DB 13;

Length 715

Query Match Best Local S Matches 19

1 Similarity 19; Conserv

Conservative

84.8%; 90.5%;

Score 17.8; DB 17 Pred. No. 9.1e+02;

DB 17;

Length 512; Indels

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RESULT 5
AQ862416/c
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Wing, R.A. and Dean, R.A.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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//tissue_type_Tical*
//tissue_type_Tical*
//lab_host="p. coli DH10B"
//lab_host="p. coli DH10B"
//lab_host="p. coli DH10B"
//note="vector: pBACINGigo; Site_1: EcoRI; Site_2: EcoRI;
//rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mpp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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/strain="Japonica"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 706)
Dunn,D., Aoyagi,A., Barber,M.,
Tinnaud
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72 AGGTGATTTGGAGATTGTGA 491
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19; Conser
                                                                                                                                                                                                                                                                         High quality sequence stop: 706.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0348 row: K column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ507082 706 bp DNA linear GSS 05-OCT-200 1M0348K01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0348K01 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                       Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ507082.1 GI:10688398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through
                                          /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XLI blue MRF"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
oligo-dT-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"
120 c 143 g 108 t 1 others
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/db_xref="taxon:7955"
/db_xref="taxon:7955"
/clone="MPMGp637_13F2;MPMGp637F0213"
/clone_lb="267"
/clone_lb="267"
/clone_lb="267"
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/clone="UUGC1M0348K01"
                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                          'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole embryo"
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 939)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGGGGATTTGGAGATTGTGA 21
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: ResGen, Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13799 row: j column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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BQ899695
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AGENCOURT 8750911 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6336113
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                                                                                                                                                   /clone_lib="NIH_MGC_130"
/lab_host="hH10B (phage resistant)"
/lab_host="hH10B (phage resistant)"
/note="forgan: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/note="forgan: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/note="forgan: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/note="forgan: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/note="forgan: otocysts; Vector: pCMV-SPORT6.1.ccdb; Vector: pCMV-SPORT6.1.ccdb; Vector: pCMV-SPORT6.1.ccdb;
/note="forgan: otocysts; Vector: pCMV-SPORT6.1.ccdb; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10000"
/clone="IMAGE:6336113"
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Pred. No. 5.
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                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq length: 0
DB seq length: 2000000000
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## ALIGNMENTS

RESULT 1 BI891021 LOCUS REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM ACCESSION VERSION COMMENT DEFINITION TITLE JOURNAL 1 (bases 1 to 527)
Clark, M., Aanstad, P., Hennig, S., Johnson, S.L. and Lehrach, H. EST sequencing of a zebrafish shield stage cDNA library normalised by oligonucleotide fingerprinting Uppublished (2001)
Contact: Hennig S
laboraty 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1862
Tex: +49 30 8413 1360 mRNA seq BI891021 BI891021 527 bp mRNA linear EST 12-OCT-2001 ZF637-3-000276 Zebrafish shield stage whole embryo cDNA library MPMGp637 Danio rerio cDNA clone MPMGp637\_13F2;MPMGp637F0213 5', Danio rerio
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
; Cyprinidae; Danio. Email: hennig@molgen.mpg.de 5' EST sequencing of clones from a zebrafish shield stage library, normalised from 55,000 starting clones by oligonucleotide fingerprinting zebrafish BI891021.1 GI:16098292 sequence. ; Craniata; Teleostei; Vertebrata; Euteleostomi; Ostariophysi; Cypriniform Cypriniformes

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RESULT 15
AAA97385/c
ID AAA97
XX AAA97
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                                                                                                                                                                                        The invention relates to a light-repressible promoter (AAA97385), or active fragments thereof (AAA97383, AAA97384), from the gene encoding the pea GTP-binding protein pra2. The invention also relates to an expression cassette containing the pra2 promoter or its active fragments for the expression of a gene under photoinhibitory or dark conditions in a plant, and to transgenic plants, their descendants and plant tissues comprising the expression cassette. The expression cassette transgenic plants in which deterioration during storage in the dark is prevented. This is particularly useful for agricultural products. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding protein pra2; pea; light-repressible photoinhibitory; expression cassette; transgenic deterioration prevention; storage; ds.
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AAA97385 standard; DNA; 2325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA97385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA fragment or promoter for expressing a target gene, specifically under photoinhibitory conditions, and for transforming a plant cell or plant to improve quality and prevent deterioration during storage \,\cdot\,
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                                                                                                                 Sequence 2325
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                                                                                                                                                                         represents the pea pra2 promoter.
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Search completed: July 8, 2003, 03:11:16 Job time : 21.9513 secs

99US-0144632. 99US-0144884. 99US-0144814. 99US-0145086. 99US-0145088. 99US-0145085.

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RESULT 14
ABLI1065/c
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XX ABLI1065;
AC ABLI106
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                                                                                                                              New isolated nucleic agenes from Drosophila interactions -
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
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RESULT 13
AAC52475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to 224 nucleic acid sequences comprising at least CC 18 bases of a chemically pretreated gene associated with gene regulation CC selected from 43 known genes (or complementary sequences). The CC chemical pretreatment converts cytosine bases unmethylated at the CC 5-position to uracil or another base with hybridisation behaviour CC dissimilar to cytosine, to enable analysis of cytosine methylations. CC useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by CC enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac constitue, preclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this specification and is cassociated with the human gene regulation associated genes. The present sequence is a format directly from WIPO at the printed specification, but was obtained in electronic committed committed specification, but was obtained in electronic committed committed specification, but was obtained in electronic committed committed specification and sequence data for this specification committed committed specification, but was obtained in electronic committed committed specification, but was obtained in electronic committed committed specification and sequence data for this specification committed specification.
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    THE PRESENTATION OF THE PR
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Best Local S
Matches 17
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

19-APR-1999

19-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16914 BP; 4573 A; 449 C; 4019 G; 7823 T; 50 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC52475 standard;
                                                                                                                                                                                                                                                                                                                    06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana DNA fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000
                                                                                                                                                                                                                                                                           25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                           2000EP-0301439
990S-0123180
990S-0123548
990S-0125788
990S-0126264
990S-0126785
990S-01267462
990S-0128234
990S-0128714
990S-0130077
990S-0130077
990S-01300449
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                                                                                                                                                                                                                                   99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO: 71461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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        06-MAY-1999
07-MAY-1999
07-MAY-1999
11-MAY-1999
11-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-013553
99US-0135692
99US-0136392
99US-0136392
99US-0137528
99US-0137724
99US-0137724
99US-0138044
99US-0138044
99US-0138847
99US-0138847
99US-0139452
99US-0139452
99US-0139452
99US-0139452
    99US-0140353.
99US-0140695.
99US-0140823.
99US-01410823.
99US-01410842.
99US-014205.
99US-014209.
99US-014209.
99US-014209.
99US-014209.
99US-014209.
99US-014209.
99US-0144086.
99US-0144332.
99US-0144332.
99US-0144332.
99US-0144333.
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99US-0134219.
99US-0134219.
99US-0134221.
99US-0134370.
99US-0134941.
99US-0135124.
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99US-0132485.
99US-0132486.
99US-0132487.
99US-0132863.
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99US-0139750.
99US-0139763.
99US-0139817.
99US-0139899.
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99US-0139459.
99US-0139460.
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99US-0139456.
99US-0139457.
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99US-0130891.
99US-0131449.
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RESULT 11
ABL70316
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, naaemia, caute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/alcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation \, -
                    Olek A,
                                                              30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                 Unidentified
                                                                                                                                                                                                Cell signalling;
                                                                                                                                                                                                                   Chemically treated cell signalling DNA sequence complementary to#103
                                                                                                                                                                                                                                                                                        ABL70316 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1435; 32pp + Sequence Listing; German.
                                                                                              29-JUN-2001; 2001WO-EP07471
                                                                                                                      10-JAN-2002
                                                                                                                                           WO200202807-A2
                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                             01-JUL-2002
                                                                                                                                                                                                                                                                    ABL70316;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13377 BP; 3915 A; 146 C; 3046 G; 6270 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002.
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                                         (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-)
                                                                                                                                                                                                                                                                                                                                              1704 TAAGGGATTTGGAGATTGTTA 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which
                                                                                                                                                                                                                                                                                                                                                                   1 TAGGGGATTTGGAGATTGTGA
                                                                                                                                                                                                                                                                                                                                                                                           19;
                                         EPIGENOMICS AG
                                                                                                                                                                                       tumour;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPIGENOMICS AG
                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention provides a number of human immune system associated are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                              2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                       cytostatic;
                                                                                                                                                                                                cytosine methylation;
                                                                                                                                                                                                                                                                                        DNA; 16914 BP
                                                                                                                                                                                                                                                                                                                                                                                                   84.8%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                    Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                   21
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                    ×,
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                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                               signalling disease
                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Length 13377;
                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 12
AAS61254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilla; Werner syndrome; asthma, HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
                                                                                              01ek
                                                                                                                                                                                           06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling -
                                                                                                                                                                                                                                                                                                                             06-APR-2001; 2001WO-EP03968
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200177375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nephrotropic; gynecological; anti-tumour; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene regulation-associated gene oligonucleotide #209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS61254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS61254 standard; DNA; 16914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16914 BP; 4573 A; 449 C; 4019 G;
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                                           WPI; 2002-017470/02
                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2002
                                                                                                                                               (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lmmunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
17; Conserv
                                                                                                                                               EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGGGGATTTGGAGATT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGGGGATTTGGAGATT 5139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                               AG
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                                                                                            Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7823 T; 50 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 16914;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic
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New nucleic acid sequences

from chemically modified

genes

associated

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RESULT 9
AAS46475
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticities, therapeutics and pharmaceutical drugs. The invendiscloses genomic DNA sequences (ABLG176-ABL30511), expressed DNA (ABB5737-ABB72072).

The sequences (ABB16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 33890; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter
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15-MAR-2001; 2001WO-EP02955
                                                                          WO200168912-A2
                                                                                                                Homo sapiens
                                                                                                                                                       cytosine
                                                                                                                                                                          cancer;
                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                  Tumour suppressor
                                                                                                                                                                                                                                                                          18-DEC-2001
                                                                                                                                                                                                                                                                                                                   AAS46475;
                                                                                                                                                                                                                                                                                                                                                    AAS46475 standard;
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                                     20-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JC,
                                                                                                                                                                          tumour suppressor gene;
tumour; CpG dinucleoti
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19; Conser
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                                                                                                                                                     methylation;
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                                                                                                                                                                                                                                  gene derived chemically modified sequence #197.
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                                                                                                                                                                          dinucleotide;
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                                                                                                                                                                        single-nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                    RESULT
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
              antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epile neurofibromatosis; rheumatoid arthritis; psoriasis; bowel
                                                                      antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid comprising a sequen bases, of a segment of chemically pretreated DNA (CP DNA) e bisulphite, of genes associated with tumour suppression and
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                                                                                                                                                                          Human
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                          system associated gene SEQ ID NO:
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                                                                                                                                                                                                                 (first
                                                                                                                                  system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                               entry)
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epilepsy;
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                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour in which a myc gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated
                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                 Claim 1; SEQ ID NO 19687; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                              specification, but was obtained in electronic
at ftp.wipo.int/pub/published_pct_sequences.
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11-JUL-2000; 2000US-0614150
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pharmaceutical;
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                                                         ABL13136 standard;
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 32840; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
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                                   ABL13136;
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                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    detection reagent for detecting for elucidating cell signalling
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                                                                                                                                                                      Score 17.8;
Pred. No. 8
                                                                                                                                                                                                        C; 533
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26-MAR-2002

(first entry)

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as oligomer probes for detecting the cytosine methylation st
single nucleotide polymorphisms (SNPs).
Note: The sequence data for this patent did not form part of
specification but is based on sequence information supplied
the European Patent Office.
                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5518 BP; 1383 A; 142 C; 1452 G; 2541 T; 0 other,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL32217 standard; DNA; 5518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune system disease; cytosine methylation;
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95.0%;
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The present invention provides a number of human genes which are modified by the methylation of cy

cytosines.

immune system associated ytosines. The sequences

treated

Claim 1;

SEQ ID

NO 190;

32pp + Sequence Listing;

German

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RESULT 5
AAA51818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC Investigation of silencing of caspase-8 (CASP8) gene by methylation was canalyzed using methylation-sensitive pcra analysis. Amplification of the CS intranslated region (UTR) of the Casp8 gene was performed in reaction mixtures containing bisulfite treated DNA. Primers AAA51819-23 were CC designed to produce a 320 bp fragment in the upstream region of Casp8 gene extending from nucleotides +221 to +541. Wild type primers were CC used to amplify the corresponding region of untreated genomic DNA. CC controls without DNA were also performed. CASP8, a cysteine protease, is CC part of the death inducing signaling complex (DISC) associated with the CC part of the death inducing signaling complex (DISC) associated with the CC tumour suppressor gene. The CASP8 promoter region sequences, in CC controls region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation. CC Methylation PCR can be used to examine even minute amounts of patient CC material to demonsrate whether the CASP8 gene expresses an mRNA and CC protein product. The CASP8 gene has been localized to human chromosome CC 1233-34. The methods are used to diagnose or prognose cancer. Cancer is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used in the diagnosis and treatment of immune system disord including eye diseases such as retinopathy, neovascular glaucoma a macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                         Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kidd VJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sense primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5518 BP; 1383 A; 142 C; 1452 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis, psoriasis and inflammadiseases. The present sequence is a gene of
treated by administering a vector that expresses a gene encoding functional CASP8 in cells. The cancer that is diagnosed or treat
                                                                                                                                                                                                                                                                                                                                                                          Example 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for CASP8 methylated-specific bisulfite treated DNA
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                                                                                                                                                                                                                                                                                                                                                                      61; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis;
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ome 2q33-34; neuroblastoma; cancer;
cytostatic; gene therapy; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOSPITAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 2
ABL54318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mixtures containing bisulfite treated DNA. Primers AAA51818-23 were containing bisulfite treated DNA. Primers AAA51818-23 were considered to produce a 320 bp fragment in the upstream region of Casp8 gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls without DNA were also performed. CASP8, a cysteine protease, is part of the death inducing signaling complex (DISC) associated with the CC part of the corresponding region complex (DISC) associated with the CC particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation.

CC particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation.

CC Methylation PCR can be used to examine even minute amounts of patient material to demonsrate whether the CASP8 gene expresses an mRNA and CC protein product. The CASP8 gene has been localized to human chromosome 243-34. The methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding cumour in which a myc gene is amplified, such as a neuroblastoma. CC uncour in which a myc gene is amplified, such as a neuroblastoma. CC uncour in which a myc gene is amplified, such as a neuroblastoma. Or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated carcinoma.
В
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                            06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Investigation of silencing of caspase-8 (CASP8) gene by methylation was analyzed using methylation-sensitive PCR analysis. Amplification of the 5 untranslated region (UTR) of the Casp8 gene was performed in reaction mixtures containing bisulfite treated DNA. Primers AAA51818-23 were
               OLek
                                                                                                                                                                                                                                                                                     neurodegenerative disorder; Herpes simplex virus; amyotrophic lateral sclerosis; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising
                                                                                                                                                         06-APR-2001;
                                                                                                                                                                                                                                                                                                                     Apoptosis; HIV; Bloom syndrome; cardiopathy,
                                                                                                                                                                                                                                                                                                                                                   Chemically treated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                     ABL54318;
                                             (EPIG-)
                                                                                                                                                                                         18-OCT-2001
                                                                                                                                                                                                                         WO200177164-A2
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                                               EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAGGGGATTTGGAGATTGTGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGGGGATTTGGAGATTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page
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                                                                            2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                             AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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                                                                                                                                                                                                                                                                                                      renal ischaemia;
                                                                                                                                                                                                                                                                                                                                                   gene
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RESULT 3
ABN80019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to chemically pre-treated DNA of genes associated with apoptosis. The nucleic acids are used to allocate patients for specific therapy for HIV infection, Bloom syndrome, cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours and cancers. This nucleotide sequence represents a chemically treated apoptosis gene. Even SEQ ID numbers are the complementary DNA strands to the odd SEQ ID numbers. The sequence data for this patent is not represented in the printed specification but is based on information supplied by the European patent office.
The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA ( of genes associated with development selected from 87 genes listed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer -
                                                                                              Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated.
                                                                                                                                                                                                                                          30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                        Claim
                                                                                                                                                                                      Olek
                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP07536
                                                                                                                                                                                                                                                                                                                  03-JAN-2002
                                                                                                                                                                                                                                                                                                                                             WO200200927-A2
                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               dwarfism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human chemically modified disease associated gene SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABN80019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5518 BP; 1383 A; 142 C; 1452 G; 2541 T; 0 other;
                                                                                                                                                                                                                 (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                              heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN80019 standard;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                      A
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                                                                                                                                                        2002-130908/17
                                                                                                                                                                                                                                                                                                                                                                                                                                             disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Seq ID #18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 TAGGGGATTAGGAGATTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TAGGGGATTTGGAGATTGTG
                                                                                                                                                                                                                 EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                        SEQ
                                                                                                                                                                                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                               ease; epilepsy; histone deacetylation; muscular dystrophy;
single nucleotide polymorphism; SNP; cytosine methylation,
tic; cytostatic; anticonvulsant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2000DE-1043826
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                                                        36;
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95.0%;
                                                     27pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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Pred. No. 48
                                                        English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOX; diabetes; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                            of genes associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO
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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on:
                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB DB
                                                                                                                                                                       Score
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18.4
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21
1 tarr
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Gapop 10.0 , Gapext 1.0
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87.6
87.6
84.8
84.8
84.8
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                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                    1: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
4: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
5: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
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17: \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
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                                                                                                                                                                                          Query
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                AAA51818
ABL22738
ABL12786
ABL13136
                                                                                   AAA51820
ABL54318
ABN80019
ABL32217
AAS46475
                                                                                                                                                                                                                            SUMMARIES
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Compugen Ltd
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                                               Chemically treated Human chemically m Human immune syste Sense primer for C Drosophila melanog
                                                                                                                                                                         Description
Drosophila melanog
Drosophila melanog
Tumour suppressor
                                                                                                                                        Sense primer for C
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nervous sys	Human nervous syst	Human nervous syst	nervous sy	metastasis	Signal transductio	Human immune syste	Human immune syste	Human immune syste	Human DNA for stag	Human immune/haema	Arabidopsis thalia	Human prostate exp	Oligonucleotide fo	Œ	መ	Human immune/haema	Genomic sequence #	ğ	I-2 contain	cter pyl	ate	ide	nucleotic		Þ	Human immune/haema	Pea light-repressi	ila melano	96	Drosophila melanog	s thali	regul	Chemically treated	ne sy

## ALIGNMENTS

RESULT 1 AAA51820 ID AAA5

AAA51820 standard; DNA;

21 BP

AAA51820;

CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; primer; ss. Kidd Sense primer 31-OCT-2000 Detecting inactivation of a caspase- $\theta$  (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA 06-JUL-2000 WO200039347-A1 Homo sapiens. 31-DEC-1998; 30-DEC-1999; (SJUD-) ST JUDE CHILDREN'S RES ٧J, 2000-452423/39. Lahti JM, (first entry) for CASP8 unmethylated-specific bisulfite treated DNA 98US-0114308 99WO-US31280 Teitz T; HOSPITAL

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/note="27 copies 2 mer aa 74% conserved"
26986 . 27049
/note="32 copies 2 mer tt 67% conserved"
27058 . 28403
/note="11PA16 repeat: matches 4771 . .6156 of consensus"
28404 . .28699
/note="Aludb repeat: matches 6 . .304 of consensus"
28700 . .29162
/note="LipA16 repeat: matches 4315 . .4771 of consensus"
2948 . .30441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2073 . .2570 of consensus"
34418 . 34526
/note="MIR repeat: matches 31 . .139 of consensus"
34653 . 34951
/note="L1ME1 repeat: matches 5827 . .6105 of consensus"
34952 . .35443
/note="L1CR1a repeat: matches 1 . .497 of consensus"
35444 . .35913
/note="L1ME1 repeat: matches 5285 . .5827 of consensus"
35955 . .36631 repeat: matches 5285 . .5827 of consensus"
36633 . .37090
                                                                                                                                                                                                                                                                                          39131. .39181

note="LTR30 repeat: matches 1. .52 of consensus"

39185. .39292

/note="pTR5 repeat: matches 1570. .1679 of consensus"

39293. .39981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31560. .33433
/note="L1MA9 repeat: matches 4436.
33796. .34254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: Em:AQ280648"
30764, .30992
/note="12129eat: matches 4435, .4668 of consensus"
                                                                                                  39982. .40184

'note="L1 repeat: matches 4715. .4912 of consensus 10338. .40650

note="Alusx repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1 repeat: matches 4553. .4718 of consensus"
38824. .39051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %770te="LIM4 repeat: matches 3548. .4026 of consensus" 37269. .37376 % 37269. .37376 % 37269. .37376 % 37510. .37705 % 37510. .37705 % 37510. .37705 % 37510. .37705 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 % 37510 %
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complement(30506 .31171)
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complement(23742. .24153)
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20099. .20355
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note="LIM4 repeat: matches 3603. .3874 of consense 0275. .20787
'note="match: GSS: Em:AQ547282"
'1667. .22029
'note="MITIB repeat: matches 4. .375 of consensus"
                                                                                                                                                                                                                                                       note="LTR12 repeat: matches 1. .671 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match: GSS: Em:AQ490802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="pTR5 repeat: matches 743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50. .38650 repeat: matches 5231.
                               e="LTR16A repeat: matches 61. .445 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e="match: GSS: Em:AQ182243"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .965 of consensus"
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50285 TAGGGGATTTGGATATGGTGA 50305
                             1 TAGGGGATTTGGAGATTGTGA 21
                                                               Conservative
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                                                                                                                                                                                                                            42069. .42189
/note="FLAM_C repeat: matches 7.
43350. .43736
                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 1777. .2128 of consensus" 41824 ..41926 //note="L1286 repeat: matches 6041. .6143 of consens 42066 //1286 repeat: matches 6041. .6143 of consens
                                                                                                                             44232. .44969
                                                                                                                                           .4214. .44643
/note="match: GSS: Em:AQ358471"
                                                                                                                                                                          /note="match: GSS: Em:AQ269706"
                                                                           84.8%;
                                                            Score 17.8; DB 9; Pred. No. 2.4e+02; 0; Mismatches 2
                                                                                                                                                                                                                                             .126 of consensus"
                                                                                            Length 98368;
                                                               Indels
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Search completed: July 8, 2003, 04:02:46
Job time: 79.7495 secs

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CBH0 1sA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 7, 2000 this sequence version replaced gi:6723337.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map roblems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
19; Conserv
                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 wasping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL136453 98368 bp DNA linear PRI 31-MAR-2000 Human DNA sequence from clone RPI-249K20 on chromosome 10. Contains STSs and GSSs, complete sequence.
1 TAGGGGATTTGGAGATTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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AL136453.3 GI:6912131
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GNKTIITISDEARDDLYKHMMDQSLAGLMGAVVINVINKKMSKSKKEHYTCHASK
NVTAHAKCVYTVLDQVKKRNEKLERFSTRASRLKHQKQQRSDGKALKNSMNYKEEVY
KSGGEEFRVKRGSGTTVEDEMENKRQAVIRENVQTRKSYELRDNKSLSPLALIARKLT
ELVRAGKNKXEPQKRWQDVIQEIKNESTRIKGKSQNKEEMKRKFSKFIRTMKGTGLNA
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/gene="Y39D8B.3"
/codon_start=1
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/protein_id="AAF60533.1"
/db_xref="GI:7331845"
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VERSION KEYWORDS SOURCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="13 con 3274.
                                                                                                                                                                                                                               /note="MIR repeat: 11677. .11813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSx repeat: matches 1. 9089. .9457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7363. .7540 /note="L1M1 repeat: matches 5381. .5563 of complement(7577. .7983)
                                                                                                                                                                  15047. .16331
/note="LIMCa repeat: matches 514.
16356. .16583
                                                                                                                                                                                                                                                                                              /note="L1MA5A repeat: matches 6043. 13736. .14644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: GSS: 2971. .2996
             /note="match: GSS: Em:AQ387926"
19193. .19596
                                                                          /note="MIR repeat: matches 11.
complement(18285. .18763)
                                                                                                        /note="MER63
18114. .18346
                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AQ270786"
13417. .13645
                                                                                                                                                                                                                                                                                                                                                                 13271
                                                                                                                                                                                                                                                                                                                                                                                               12899
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluY repeat: matches 165. .301 of consensus"
12588. .12886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10062.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                  /note="MER34 repeat: matches 190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9284. .9371
/note="8 copies 11 mer 68% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="61 copies 2 mer aa 63% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="MIR repeat: matches 2. .192 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ≈"9 copies 4 mer caca 97%
.4317
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                                                                                                          ERRO3 repeat: matches 979. .1046 of consensus"
18346
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13407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 2666. .2747 of consensus"
                                                                                                                                                      repeat: matches 3909.
repeat: matches 952. .1353 of
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Submitted (24 MAY-2002) Department of Genetics, Washing University, Genome Sequencing Center, 4444 Forest Park Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MO 63108,
5 (bases
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Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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2 (base
                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-FEB-1999) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 20303)
Becker, M., Graves, T. and Yc
The sequence of C. elegans
Unpublished (2001)
3 (bases 1 to 20303)
                                                                                    The 5' cosmid is T22H9, 3951 bp overlap; the 3' cosmid is ZK6, 200 bp overlap. Actual start of this cosmid is at base position 31064 of Y58G8A; actual end is at 27075 of F48G7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not be the entire insert of this clo
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-MAR-2000)
University, 4444 Forest
6 (bases 1 to 20303)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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Eukaryota; Metazoa; Ne
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                                                                                                                                                                                                                   http://www.wormbase.org/db/seq/sequence?name=Y39D8B;class=Sequence
                                                                                                                                                                                                                                          analysis see:
                                                                                                                                                                                                                                                            For a graphical representation of this cosmid sequence and its
                                                                                                                                                                                                                                                                                                          more than one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           neighboring submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Genetics, Washington St. Louis , MO 63110, USA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Sequencing Center
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  the result
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integration
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6844. .713
                                                                                                                        RQNVSEMYGDYKTSKIDSMEKLHKSMSAAQMHEMNSTGYAIMSSQQISEFYGPGSPYN
DSHAYENYRNLRRNDIPDILENNIHQMAREEQAFKVARQVGRELMRTTHYKNFQISRK
M"
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                                                                                                                                                                                                                                                                                     FSLIAKTLIDIVRENKNKEKEPKKKWQTVINEIKDELNRIKQKKKDQEDFRNYFSKYS
RTMKKLGLNPETAFRRAGLDSIGEELSAANTTGKLSEEGQVLKKPLMMIRDGVKLGAM
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RAMRFLSENGHDDWMNFVLEASGVTEAVEKMRFDERKQEMEAFRKHFSNENGQPMYFT
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                                                      .19960)
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18; Conser
                                                                                                                                                                                                                                                                                                                                           Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishi,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kimura,K., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T., NEDO, human cDNA sequencing project
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                                                 19;
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Homo sapiens fetal brain cDNA to mRNA, clone_lib:OCBBF2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Isogai, T. and Yamamoto, J.
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1 (bases 1 to 13377)
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AC006749 20303 bp DN/
Caenorhabditis elegans cosmid Y39D8B,
AC006749
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                                                                                                                                                             1 TAGGGGATTTGGAGATTGTGA 21
                                                                                                                                                                                                l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with the Patent: WO 0200928-A 1435 03-JAN-2002;
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synthetic construct
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197 from Patent WO0168912.
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
146 c 3046 g 6270 t
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/db_xref="taxon:32630"
/note="chemically treated genomic 146 c 3046 g 6270 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 179686)
Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6904
Center clone name: 390_G_24
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Insert size: 177880; sum-of-contigs
Quality coverage: 3.9 in Q20 bases;
Quality coverage: 3.9 in Q20 bases;
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1270 2277:
2278 2377: gap
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2378. .3411
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96190. .108632
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/clone_lib="RPCI-11 Human Male
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/db_xref="taxon:9606"
                                                /note="assembly_fragment"
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179686: contig of
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79729: contig of 12392 bp in
129: gap of 100 bp
96089: contig of 16260 bp in
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7487:
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6: contig of 14221 bp in
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contig of 2368 bp
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contig of 10328 bp in length
p of 100 bp
contig of 12629 bp in length
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DOE Joint Genome Institute and Stanford Human Genome
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168250. .176144
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152502. 158391
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47260. .81942
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199642, 214787
/note="assembly_name:Contig9"
49921 c 49241 g 57431 t
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158492 ...162895
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186518. .199541
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176245. .186417
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16059. .47159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_name:Contigl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="RP23-326J1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="UNK"
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9: contig of 5154 bp in length
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4: contig of 7895 bp in length
7: contig of 10173 bp in length
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of 5890 bp in
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                                                                                                Euteleostomi;
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AUTHORS
TITLE
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AUTHORS
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ORGANISM
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AC023987/c
LOCUS
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Best Local Similarity
Matches 18; Conserv
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2 (bases 1 to 179686)
3 (birren,B., Linton,L., Nusbaum,C., Lander,E., Boguslavkly,L.,
4 (bases), Baldwin,J., Barna,N., Beda,F., Boguslavkly,L.,
5 (bases), Baddwin,J., Barna,N., Beda,F., Boguslavkly,L.,
5 (colangelo,M., Collins,S., Collymore,A., Cooke,P.,
6 (choepel,Y., Colangelo,M., Collymore,A., Cooke,P.,
6 (choepel,Y., Colangelo,M., Forrest,C., Gage,D.,
7 (colangelo,M., Forrest,C., Gage,D.,
8 (collymore,A., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
6 (calgan,J., Landers,T., Johnson,R., Johes,C., Kan,L., Karatas,A.,
8 (klein,J., Landers,T., Largocque,K., Lehoes,C., Kan,L., Karatas,A.,
8 (klein,J., Landers,T., Largocque,K., Lehoes,V., Levine,R.,
8 (klein,J., Landers,T., Largocque,K., Lehoes,V., McCartty,M.,
8 (klein,J., McGurk,A., McKernan,K., McPheeters,R., Mellrim,J.,
8 (klein,J., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
8 (klein,J., O'Neil,D., Olivar,T.M.,
8 (klein,J., O'Neil,D., Olivar,T.M.,
8 (klein,J., Olivar,T.M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC023987 179686 bp DNA linear Homo sapiens chromosome 5 clone RP11-390G24 map 5, SEQUENCE, 19 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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100.0%;
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Pred. No. 1.8e+(
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Mismatches

Indels

0;

Gaps

HTG 24-AUG-2002 WORKING DRAFT

1.8e+02

В 80

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www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 153kb). It is clipped at the overlaps with AC022139 and AC109455. The number of bases overlapped with AC022139 is 12649 and with AC109455 is 3639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-JUN-2001) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA (bases 1 to 70122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 31, 2002 this sequence version replaced gi:14333874. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                        /clone="RP11-329N11"
11786 c 12143 g 22723
                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
Length 70122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AluSp/q"
complement(9914..10340)
/rpt_family="L2"
10749..1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MIR"
complement(4701, .4881)
/rpt_family="1"
                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alusg"
complement(13500. .13642)
/rpt_family="".1"
 /rpt_family="MIR" complement(19411. .19606) /rpt_family="MIR" 19725. .19777
                                                                                                                                                                                   /rpt_family="Alusx"
17097. .17142
                                                                                                                    complement(18645. .18755)
/rpt_family="MIR"
                                                                                                                                                                                                                                                              complement(13659...13955)
/rpt_family="AluSp"
                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
complement(12321...12
                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(11241. .11322)
/rpt_family="L2"
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complement(7333. .7638
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/rpt_family="Alusx"
                                                                                                                                                                                                                                          /rpt_
14693
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7940. .8083
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                                                                                                                                             /rpt_family="L1ME4A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Charlie8"
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                                                                                                                                                             /rpt_family="(CA)n"
17949. .18097
                                                                                                                                                                                                                           rpt_family="(TTTA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="single clone coverage"
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3. 7847
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lement(1267)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _family="Alusx"
lement(8640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _family="Aluy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _famil
                                                                  _family="FLAM_C"
                                                                                                                                                                                                                                                                                                                                                                                                                _family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="MLT1J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="AT_rich"
                                                                                                                                                                                                                                                    family="(CAAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family="Charlie8"
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VERSION
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AC123853
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DEFINITION
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Matches
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                                                                                                                                                                                                                                                                                                Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 207948 bases at least Q40
Consensus quality: 208444 bases at least Q30
Consensus quality: 208788 bases at least Q20
Insert size: 171000; agarose-fp
Unality coverage: 11.36 in Q20 bases; agarose-fp
Quality coverage: 9.45 in Q20 bases; sum-of-contigs
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Mus musculus chromosome UNK clone RP23-326J1, WORKING DR
SEQUENCE, 12 unordered pieces.
AC123853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteléostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (hases 1 to 214787)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: M_BA0326J01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: submissions@watson.wustl.e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
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McPherson, J.D.
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HTG; HTGS_PHASE1; HTGS_1
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                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
      15959
16059
47160
47260
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20537. .20556
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20135. .20247
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15958: contig of 15958 bp in length
16058: gap of unknown length
47159: contig of 31101 bp in length
47259: gap of unknown length
81942: contig of 34683 bp in length
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95.0%; Pred. No. 1.2,
tive 0; Mismatches
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N., Hagos, B., Horton, L., Evine, R., Linders, T., Lehoczky, J., Levine, R., Lindelad-Toh, K., Liu, G., MacLean, C., Maddonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
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Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 188868)
Birren,B., Nusbaum,C. and Lander,E.
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172097. 186048
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136514. .140443
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O'Neil,D., Oliver,J., Peterson,K., Phunkhay, P.,
Peterson,K., Phunkhay, P.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., R., Peterson, R.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Starty-Thomann,N.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Starty-Thomann,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 1, 2002 this sequence version replaced gi:21591935.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6735
Center clone name: 793_I_11
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1098. .1295
/rpt_family="Alusp"
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Mus musculus chromosome 10 clone RP24-29317, complete sequence.
AC121986
AC121986.2 GI:22296788
                                                                                                                                                                                                           186048 bp DNA linear HTG 10-. Homo sapiens chromosome 11 clone RP11-465124, WORKING DRAFT SEQUENCE, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 182686)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
                                                                                                                                                Homo
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Mammalia; Eutheria;
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            2 (bases 1 to 186048)
Waterston, R.H.
                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 186048)
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                                                              The sequence of Homo sapiens clone
                                                                               Waterston, R.H.
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On Sep 10, 2000 this sequence version replaced gi:9931959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
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172996: gap of unknown length
186048: contig of 13952 bp in le
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/rpt_family="AluJo"
complement(9819. .9959)
/rpt_family="L2"
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                                                                                         Similarity
                                                                            Conservative
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/rpt_family="MIR"
10740. .10923
                                                                                                                                  /rpt_family="AluSx"
complement(25722, .25905)
/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                                                             complement(21371. .../rpt_family="Alusx" 22147. . . 22445
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complement(12619. .12834)
/rpt_family="MER30"
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/rpt_family="L2"
                                                                                                                                                                                                           /rpt_family="THE1B" 23617. 2360"
                                                                                                                                                                                                                                      complement(23265.
                                                                                                                                                                                                                                                                                                   /rpt_family="Alusx" complement(22969
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/rpt_family="MIR"
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complement(15717. .
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19987. .20282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="Alusc"
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                                                                                         87.6%;
95.0%;
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                                                                                       Score 18.4; DB 9, Pred. No. 1.2e+02
                                                                            Mismatches
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                                                                                                                                       Olek, A., Piepenbrock, C. and Berlin, K.
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo 142 c 1452 g 2541 t
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/note="chemically treated genom
142 c 1452 g 2541 t
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Boukhgaller, B. Brown, A. Camarata, J. Campopisno, A. Chang, J.
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
MacLean, C., Wacdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., WcEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihoya, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Riaback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Restti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Sewary, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, M., Subramanian, A., Talamas, T., Tesfave, S., Theodore, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Erown, A., Camarata, J., Camppiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Goldes, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N., Jones, G., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karratas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levne, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCeanthy, M., McZernan, K., McPheeters, R., Meldrin, J., McCarthy, M., McZernan, C., Mapphy, T., Naylor, J., Ngyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Reback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainon, J., Zaimon, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 TAGGGGATTAGGAGATTGTG 65
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
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19; Conser
                                   Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S. Topham, K., Travers, M., Travis, N., Trigilio, J., Vass Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-NOV-2001) Whitehead Institute/MIT Center for Genome
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Homo sapiens
Direct Submission
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                                                                                 Vassiliev,H.,
,W.J., Young,G.,
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. a O O 0000 000 C O O Score 16 16 16 16 Query Match .6 136372 6 182686 6 188668 6 188868 6 214787 7 70122 7 179686 6 313377 20303 98368 11529 11529 11529 11529 11529 11628 11608 11608 11653 11653 11683 Length DB AX281276 AX344611 AX345119 AC103828 AC074190 AC123853 AC091938 AC091938 AC091938 AC091938 AC09194 AX346364 AC0106749 AX346364 AC019814 AC0106749 AL13926 AC1010695 AC010695 AC010696898 AC0106923 AC026219968455 AL683819 AL6936353 AC009233 AC009233 AC009233 AC109923 IJ AX348748 AP004132 AP004998 AC104166 AC096922 G50981 A1844490 Mus muscu AL671848 Mouse DNA AC025520 Homo sapi AC116590 Mus muscu AL596455 Mus muscu AL688819 Mus muscu AL688919 Mus muscu AL689022 Homo sapi AC127994 Rattus po AL596096 Mouse DNA AX251933 Sequence AX348748 Sequence AX348748 Sequence AX348748 Sequence AX04154 Oryza sat AC104166 Homo sapi AC096922 Homo sapi AC096922 Homo sapi G50981 SHC-80091 AY094031 Arabidops AY094031 Arabidops AX281276 Sequence AX344611 Sequence AX345119 Sequence AX345119 Sequence AC103828 Homo sapi AC121986 Mus muscu AC074190 Homo sapi AC02332 Homo sapi AC02332 Homo sapi AC023387 Homo sapi AC023987 Homo sapi AC013981 Homo sapi AX09637 Homo sapi AX09637 Homo sapi AX013643 Human DNA AC019814 Drosophil AC010695 Drosophil AC010695 Drosophil AC010695 Drosophil AC010574 Drosophil AC010575 Homo sapi AC010575 Homo sapi Description Homo sapi Homo sapi

## ALIGNMENTS

	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX281276	RESULT 1
Epigenomics AG (DE)	Patent: WO 0177164-A 18 18-OCT-2001;	Diagnosis of diseases associated with apoptosis	Olek, A., Piepenbrock, C. and Berlin, K.	1	artificial sequences.	synthetic construct	synthetic construct.		AX281276.1 GI:16608531	AX281276	Sequence 18 from Patent WO0177164.	AX281276 5518 bp DNA linear PAT 02-NOV-2001	•	

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GENERAL INCOMPANION
GENERAL INCOMPANION
APPLICANT: IUCHI, SATOSHI
APPLICANT: KOBAYASHI, MASATOMO
APPLICANT: KOBAYASHI, KAZUO
ITITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN
ITITLE OF INVENTION: CLEAVAGE ENZYME GENE
FILE REFERENCE: 3914 3
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US/09/758,269
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: JP 2001-003476
PRIOR FILING DATE: 2001-01-13
NUMBER OF SEQ ID NUMBER: JP 2000-010056
PRIOR FILING DATE: 2000-01-13
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 9
LENGTH: 1734
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1731)
US-09-758-269-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/60,598
PRIOR EILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2342
LENGTH: 810
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; ORGANISM: Bacillus licheniformis
US-09-974-300-2342
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US-09-974-300-2342/c
US-09-974-300-2342/, Application US/09974300
; Patent No. US20020146721A1
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US-09-758-269-9/c
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APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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85.0%; Pred. No. 1.3e+03;
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    Length 1734;
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Search completed: July 8, 2003, 06:04:14 Job time : 31.1402 secs

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US-08-781-986A-1583/c
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Patent NO. US20020169297A1
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: USEN Susheng
APPLICANT: XIE, Mingtang
TITLE OF INVENTION: Genetic Insulator for Preventing Influence By Another Gene
FILE REFERENCE: 050229-0287
CURRENT APPLICATION NUMBER: US/09/973,945A
CURRENT APPLICATION NUMBER: 000241,735
PRIOR APPLICATION NUMBER: 60/241,735
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 37
CORTUNED DATE: 7000-10-20
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1583, Application US/08781986A Publication No. US20030054436A1
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LENGTH: 29
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                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               STREET: 9410 CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Staphy
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                               APPLICATION NUMBER: US/08/781,986
                                                                                                                                                                                                                                                                                                            COUNTRY:
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  Human
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                                                                                                                                                                                                                                                                                                                                                                                Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus Polynucleotides and Sequences
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   PB248PP
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Pred. No. 7
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APPLICANT: Farr, Spencer B.
APPLICANT: Pickett, Gavin G.
APPLICANT: Neft, Robin Eileen
APPLICANT: Neft, Robin Eileen
APPLICANT: Dunn, II, Robert Thomas
TITLE OF INVENTION: CANINE TOXICITY GENES
FILE REFERENCE: 40074200020
CURRENT APPLICATION NUMBER: US/09/911,904
CURRENT FILING DATE: 2002-04-09
PRIOR REPLICATION NUMBER: US 60/220,057
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 386
SOFTWARE: PastSEQ for Windows Version 4.0
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US-09-911-904-331
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                 SEQ ID NO 331
LENGTH: 116
TYPE: DNA
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 216
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APPLICANT: Picket
APPLICANT: Neft,
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Best Local
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TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1583
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pickett, Gavin G.
APPLICANT: Neft, Robin Elleen
APPLICANT: Dunn, II, Robert Thomas
TITLE OF INVENTION: CANINE TOXICITY GENES
FILE REFERENCE: 400742000200
CURRENT APPLICATION NUMBER: US/09/911,904
CURRENT FILING DATE: 2002-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR EPPLICATION NUMBER: US 60/220,057
PRIOR FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 116
TYPE: DNA
ORGANISM: Canis familiaris
ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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l Similarity 94.1%;
l6; Conservation
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17; Conserv
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85.0%;
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Pred. No. 1
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Pred. No. 9.6e+02;
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US-10-239-676-162/c
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Best Local S
Matches 18
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SEQ ID NO 2486
LENGTH: 1899
                                      2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 162
LENGTH: 15306
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR TILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                        FEATURE:
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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OZAKI, AKIO
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81.8%; Pred. No. 9.4e+02;
tive 0; Mismatches 4;
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US-09-973-945A-25
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                      APPLICANT: University of Kentucky Research Foundation
APPLICANT: GEN, Susheng
APPLICANT: XIE, Mingtang
APPLICANT: University Insulator for Preventing Influence By Another Gene
FILE REFERENCE: 050239-0287
CURRENT APPLICATION NUMBER: U5/09/973,945A
CURRENT APPLICATION NUMBER: 60/241,735
PRIOR APPLICATION NUMBER: 60/241,735
PRIOR APPLICATION NUMBER: 60/241,735
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 29
TYPE: DNA
Applicant Application of the control of t
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN Ver: 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09973945A Patent No. US20020169297A1 GENERAL INFORMATION:
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Best Local Similarity 81.8%;
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3309400
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2400809 CGCATAGCCACATTCGAAATGA 2400830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tocal Similarity 81.8%; es 18; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8794 CGAACATCTACATTTTAAACGA 8773
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TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANDO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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 Mismatches

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Pred. No. 4.6e+02;
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Pred. No. 1
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 2909
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-168
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                                                                             ; ORGANISM: Aspergillus US-10-128-714-5168
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US-10-128-714-5168/c
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
Query Match
Best Local Similarity
                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 5168
LENGTH: 3224
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Best Local
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamuddo, Carlos
APPLICANT: Zamuddo, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastian M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-08-31 NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8603
                                                                                                                                TYPE: DNA
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18; Conserv
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Tishkoff, Danie
Zamudio, Carlos
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85.7%;
                                                                                                  fumigatus
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Pred. No. 5.
Score 16.2;
Pred. No. 5.
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  DB 9;
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                     Length 3224;
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US-09-974-300-1167; Sequence 1167, Application; Patent No. US20020146721A1; GENERAL INFORMATION:
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; ORGANISM: Drosophila melanogaster
US-10-108-605-70
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                                                                                                                                  ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1167
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CURRENT APPLICATION NUMBER: US/10/108,605

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 09/761,142

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/176,418

PRIOR FILING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 361

NUMBER OF SEQ ID NOS: 361
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                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1167
LENGTH: 1356
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Best Local 9
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                                                       Matches
                                                                          Best Local
                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCOD
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 8481
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5. US20020160934A1
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1 CGTATATCTACATTCGAAACGA 22
                                                       18;
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                                                       Conservative
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                                                                          70.9%;
81.8%;
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85.7%; Pred. No. 6.2e+02;
% Mismatches 3;
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                                                                          Score 15.6; DB 10
Pred. No. 9.1e+02;
                                                     Mismatches
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                                                                                             DB 10;
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                                                                                          Length 1356;
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                                                     Indels
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                                                     Gaps
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Minimum
Maximum
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Perfect score:
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DB seq length: 2000000000
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       nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
     Published_Applications_NA: *
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
     2919
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                                                                                                                                                                                                                                                                          Length
 9 US-09-738-626-1486
9 US-10-239-676-162
9 US-09-738-626-1
9 US-09-973-945A-25
9 US-09-973-945A-26
7 US-08-781-96A-1583
9 US-09-911-904-216
9 US-09-911-904-231
10 US-09-911-904-231
10 US-09-974-300-2342
10 US-09-758-269-9
9 US-10-239-676-78
9 US-10-239-676-78
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US-10-128-714-168
US-10-128-714-5168
US-10-108-605-70
0 US-09-974-300-1167
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Sequence 2471, Ap
Sequence 5168, App
Sequence 5168, App
Sequence 70, Appl
Sequence 2486, App
Sequence 162, Appl
Sequence 152, Appl
Sequence 25, Appl
Sequence 216, Appl
Sequence 216, Appl
Sequence 217, App
Sequence 2342, App
Sequence 2342, Appl
Sequence 117, App
Sequence 177, App
Sequence 117, App
Sequence 114, Appl
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US-09-803-719-19	05-09-764-891-6605 0-764-877-3194	US-10-091-572-469	US-09-764-891-6051	US-09-764-891-5648	US-09-764-868-1285	US-10-239-676-120	US-10-239-676-23	US-09-089-818B-6	US-10-071-766-39	US-09-994-485-7	US-09-832-292-11	US-09-801-368-373	US-10-093-037-11	) US-10-121-032-11 Seq	US-10-093-037-57	US-10-121-032-57	US-10-198-846-13846	US-09-893-519A-116	US-09-938-842A-4152	US-09-974-300-4075	US-10-105-613-412	US-09-747-377-412	US-09-771-208-20	US-10-109-551-3
Sequence 19, Appl	Sequence 5505, Ap Sequence 3194, Ap	Sequence 469, App	Sequence 6051, Ap	Sequence 5648, Ap	Sequence 1285, Ap	Sequence 120, App	Sequence 23, Appl	Sequence 6, Appli	uence	quenc	luence	gueno	luence	[uence	luence	[uence	nence	nence	uence 415	quence 40	uence 412,	Sequence 412, App	Sequence 20, Appl	Sequence 3, Appli

## ALIGNMENTS

US-09-938-842A-2471

GENERAL INFORMATION:

Sequence 2471, Application US/09938842A Patent No. US20020160378A1

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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR EILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2471
LENGTH: 2919
TYPE: DNA
US-10-128-714-168/c
; Sequence 188, Application US/10
; Publication No. US20030119013A1
; GENERAL INFORMATION:
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                                                                                     RESULT 2
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                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                       Local
                                                                                                                                              78.2%; Score 17.2; DB 9; 1 Similarity 86.4%; Pred. No. 1.9e+02; 19; Conservative 0. M:cm.--
                                           US/10128714
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APPLICANT: L1, SOMMUL:
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 633
LENGTH: 630
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(630)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-633

AC 4%: Score 14.6; DB 4; Length 630;
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US-09-605-785-633/c
Search completed: July 8, 2003, 05:56:44
Job time: 27.2769 secs
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patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                   Query Match 66.4%; Score 14.6; DB 4; Length 630; Best Local Similarity 81.0%; Pred. No. 1.6e+02; Matches 17; Conservative 0; Mismatches 4; Indels
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366 GTATATCTACATTCCTATTGA 346
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Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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US-08-779-379-23
                                                                                                                                RESULT 13
US-08-469-219-23
                                                                                                                                                                                                                                                                                                                                 : HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-779-379-23
                            Sequence 23, Application US/08469219
Patent NO. 5863534
GENERAL INFORMATION:
APPLICANT: Reclon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5858970
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                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,44
FILING DATE: 08-APR-1994
ATTORNEY_AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,379
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: INVEL PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 469 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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T: 30 Rockefeller Plaza
New York
                                                                                                                                                                                                CGCATATCAACATTCAAAATG 447
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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NOVEL POLYPEPTIDE HAVING FACTOR XA
INHIBITORY ACTIVITY
                                                                                                                                                                                                                                                                                 66.4%;
NOVEL POLYPEPTIDE HAVING FACTOR XAINHIBITORY ACTIVITY
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                                                                                                                                                                                                                                                                                 Score 14.6;
Pred. No. 1
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                                                                                                                                                                                                                                                                                ; DB 2;
1.6e+02;
                                                                                                                                                                                                                                                                                                Length 469;
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                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: of clone pSP65-XaI-4. US-09-228-152-23
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-228-152-23
                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/228,152
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR XA INHIBITORY ACTIVITY
FILE REFERENCE: 43020aya
                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09228152
Patent No. 6211341
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 base pairs
TYPE: nucleic acid
                                                                                                                       LENGTH: 469
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEPAX: 212-664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,219
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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             66.4%;
81.0%;
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81.0%;
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Pred. No. 1.
             Score 14.6;
Pred. No. 1.
Mismatches
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          1.6e+02;
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                                DB 4;
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                              Length 469;
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Gaps

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RESULT 10
US-08-226-264-25
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REGISTRATION NUMBER: 0317,

REFERENCE/DOCKET NUMBER: 0317,

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-977-9550

TELEPAX: 212-664-0525

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 469 base pairs
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-FOS

SOFTWARE: PATENTIN PC-DOS/MS-FOS

SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/226,264

FILING DATE: 08-APR-94

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 40017-A/JPW/GJG

TELECOMMUNICATION INFORMATION:

TELECHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Goldlust, Arie
APPLICANT: Righi, Meir
APPLICANT: Panet, Amos
APPLICANT: Fischer, Meir
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT FACTOR XA
TITLE OF INVENTION: INHIBITORS OF LEECH HIRUDO MEDICINALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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Local Similarity 81.08;
les 17; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08226264
                                                                                                                                                                                                                                                                                                                                                                             E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levanon, Avigdor
Guy, Rachel
Goldlust, Arie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Werber, Moshe M.
Zeelon, Elisha P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0317/43020-A/JPW/EAB
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                                                              ; ANTI-SENSE: NO; FRAGMENT TYPE: US-08-467-389-23
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US-08-467-389-23
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Best Local :
Query Match
Best Local Similarity 81.0
Matches 17; Conservative
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APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POL
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                        TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: 1
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LENGTH: 469 base pairs
                                                                                                                                                                                                                                                                                    FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 469 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York ZIP: 10112
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30 Rockefeller Plaza
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                                                                               N-terminal
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                                                                                                                          DNA (genomic)
                                                                                                                                                          single
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                  66.4%;
81.0%;
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Pred. No. 1.
                Score 14.6; DB 1; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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.6e+02;
                              Length 469;
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Indels

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Gaps

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; NAME/KEY:
; LOCATION:
US-08-975-703-5
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                                                                                                                                                                          Sequence 5, Application US/09515884 Patent No. 6235263 GENERAL INFORMATION: APPLICANT: Wong, Alexander K.C.
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/975
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A
REGISTRATION NUMBER: 38,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wong, Alexander K.C. APPLICANT: Bartel, Paul L. APPLICANT: Teng, David H.-F. APPLICANT: Tavtiglan, Sean V. TITLE OF INVENTION: A Carboxy-TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-783-6031 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-784-1589
TELEPAX: 202-783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CI
HYPOTHETICAL: NO
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ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: ADDRESSE: Rothwell, Figg, Ernst & Kurz, P.C.
ADDRESSEE: 8555 Thirteenth Street, N.W., Suite 701 East
                                                                                                                                                                                                                                                                                                                                2 GTATATCTACATTCGAAA 19
|||||||||| ||| ||||
1103 GTATATCTAGATTAGAAA 1120
                                                                               TITLE OF INVENTION: A Carboxy-Terminal BRCAl Interacting Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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16; Conserv
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: DC
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1..2691
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                                                                                                                                     Bartel, Paul L.
Teng, David H.-F.
                                                                                                                     Tavtigian, Sean V.
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88.9%;
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Pred. No. 1
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2;
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US-08-468-347-23
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                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Appl Patent No. 578342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ZeeLon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-624-1589
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 5:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL FOLYPEPTIDE HAVING FACTOR XA
TITLE OF INVENTION: INHIBITORY ACTIVITY
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                 STATE: New York ZIP: 10112
                                                                                                                                                    STREET: 30 Roc
CITY: New York
                                                                                                                                                                        ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,884
FILING DATE: 29-Feb-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/975,703
ETILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1103 GTATATCTAGATTAGAAA 1120
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ORGANISM: Homo sapiens
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2694 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Saxe, Stephen A. REGISTRATION NUMBER: 38,609
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STATE: DC
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1..2691
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88.9%;
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Pred. No. 1.4e+02;
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                    Version #1.25
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                                                                                 NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
RETERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEPAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09134078 Patent No. 6368844 GENERAL INFORMATION:
                                                                                                                                                                                                                  OPERATING SYSTEM: WINDOWS95
SOFTWARE: FASKEDQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFICATION 13-AUG-1998
APPLICATION NUMBER: 08/949,026
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-CVT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hails Tirormation:
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Best Local Similarity 88.9
Matches 16; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 2018 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: misc_feature NAME/KEY: misc_feature LOCATION: 1...2018
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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HYPOTHETICAL:
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ADDRESSEE: Gray Cary
STREET: 4365 Executi
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MEDIUM TYPE: Diskette
 MOLECULE TYPE:
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STRANDEDNESS: GOULD
TOTOLOGY: Circular
TOTOLOGY: Circular
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                              LENGTH: 2043 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Diego
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                  TOPOLOGY:
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               linear
Genomic DNA
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RESULT 7
US-08-975-703-5
; Sequence 5, Application US/08975703
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; LOCATION:
US-09-134-078-11
                                                                                                                                Query Match
Best Local Similarity
Watches 16; Conserv
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US-08-914-999-7
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Patent No. 6346406
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Best Local
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TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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APPLICANT:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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APPLICATION NUMBER: US/08/914,999 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: AND METHODS OF USE THEREFOR
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                                                                                                                                                                                                                                                                    TYPE: LL STRANDEDNESS: QUU
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STATE: New Jersey
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                                                                                     1745 GTATATTTACATTCCAAA 1728
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                                                                                                                 2 GTATATCTACATTCGAAA 19
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                                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                     2237 base pairs
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Hait, William N.
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                                                                                                                                               Conservative
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88.9%;
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Pred. No. 1.4e+02;
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Pred. No. 1.
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                                                                                                                                                                        4; Length 2237;
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US-09-134-078-57; Sequence 57, Application, Patent No. 6368844
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Best Local Similarity
Matches 17; Conserv
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LENGTH: 4212 base pairs
TYPE: nucleic acid
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
                                                                                                                                                         ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                           STREET: 4000
CITY: San Diego
STATE: CA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 1650-813-5600
TELEPHAX: 550-494-0792
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APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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TELEFAX: 706141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 23-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09134078
                                                                                                                                                                                                                                                                                                                        E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600
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1...4212
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31-DEC-1997
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85.0%;
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ER: 27:
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Pred. No. 95;
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US-09-221-017B-1034/c
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US-09-134-078-57
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Patent No. 6444799
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Best Local :
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INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1992 base pairs
                                                                                                                                                                                                    APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
DECICATION DATA:
DECICAT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                          APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                          APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
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REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEFAX: 858/677-1465
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APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
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NAME: Monroy, Glady REGISTRATION NUMBER:
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Local Similarity 88.9%;
es 16; Conservative
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Pred. No. 1.
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Mismatches

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   seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1,
2: //cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/l/ina/5B_COMB.seq:*
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US-09-134-001C-1178
US-09-221-017B-59
US-09-134-078-57
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US-09-134-098-11
US-08-914-999-7
US-08-915-884-5
US-08-915-884-5
US-08-468-347-23
US-08-268-264-25
US-08-467-389-23
US-08-467-389-23
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US-08-467-152-23
US-08-467-1631
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US-08-471-068-1
US-08-471-068-1
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RESULT 2 US-09-221-017B-39/c US-09-221-017B-39/c Sequence 39, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION: PAPPLICANT: ROSS, Bruce C. TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120 CORRESPONDENCE ADDRESS: ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto CITY: Palo Alto COUNTRY: USA COUNTRY: USA ZIP: 94304-1018 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows	Query Match Best Local Similarity 85.0%; Pred. No. 87; Bust Local Similarity 85.0%; Pred. No. 87; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 3 TATATCTACATTCGAAACGA 22 Qy 3 TATATCTACTACTACTACTACAAACGA 489	RESULT 1  US-09-134-001C-1178/c    Sequence 1178, Application US/09134001C   Patent No. 5380370   GENERAL INFORMATION:   APPLICANT: Lynn Doucette-Stamm et al	C 28 14.4 65.5 607 1 US-08-061-314A-1 Sequence 1, Appli c 29 14.4 65.5 711 4 US-09-134-001C-1834 Sequence 1834, Ap c 30 14.4 65.5 2661 4 US-09-134-001C-1659 Sequence 1834, Ap 1 14.4 65.5 5055 4 US-09-242-632A-13 Sequence 13.7 Appli c 31 14.4 65.5 5055 4 US-09-242-632A-13 Sequence 13.7 Appli c 32 14.2 64.5 213 4 US-09-134-001C-1113 Sequence 13.7 Appli c 35 14.2 64.5 422 4 US-09-134-001C-599 Sequence 113.7 Appli c 35 14.2 64.5 60.9 4 US-09-615-192A-189 Sequence 2.7 Appli c 36 14.2 64.5 60.9 4 US-08-68-072-2 Sequence 2.7 Appli c 39 14.2 64.5 60.9 4 US-08-690-721-2 Sequence 2.7 Appli c 39 14.2 64.5 836 4 US-09-221-017B-878 Sequence 2.7 Appli c 39 14.2 64.5 1314 4 US-09-134-001C-581 Sequence 878, Appli c 42 14.2 64.5 1812 2 US-08-699-536-1 Sequence 470, Appli c 42 14.2 64.5 3030 4 US-09-134-001C-470 Sequence 470, Appli c 42 14.2 64.5 3030 4 US-09-693-146-3 Sequence 1, Appli c 42 14.2 64.5 3927 4 US-09-293-238B-1 Sequence 1, Appli c 42 14.2 64.5 3927 4 US-09-293-238B-1 Sequence 1, Appli c 42 14.2 64.5 3927 4 US-09-293-238B-1 Sequence 1, Appli c 42 14.2 64.5 3927 4 US-09-293-238B-1

OPERATING SYSTEM:

Windows

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ACCESSION
VERSION
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AQ311480
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AUTHORS
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SOURCE
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nes 18; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 639)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project
                                         9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                   Contact: Shaying Zhao, William Nie.
Department of Eukaryotic Genomics
The Institute for Genomic Research
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CITBI-E1-2526L19.TR CITBI-E1
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AQ311480.1 GI:4039833
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                                                                                                                                                                  Unpublished (1998)
                                                                                                                                                                                        Map Building
                                                                                                                                                                                                           Use of a random human BAC End Sequence Database for
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\label{local_composition} hbe @tigr.org \\ are availabe from Research Genetics (info@resgen.com).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBrcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size blas. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TLB=QG_ABCDI lettuce salinas
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/clone="QGI6M15"
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/lab_host="E.coli"
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/cultivar="Salinas"
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90.08;
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                                                                                                                                                                                                                                                                               FEATURES
                                                        Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                              source
206
                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seg primer: M13 Reverse Class: BAC ends.
                           3 TATATCTACATTCGAAACGA 22
                                                                                                                                                                                                                                                                                                                                   end search page:
TATATCTATATTCGAAACTA 225
                                                                                                                                205 a
                                                          Conservative
                                                                                                                             /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
122 c 142 g 170 t
                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2526L19"
                                                                                                                                                                                                                                                                1. .639
                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                       /clone_lib="CITBI-El"
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                      76.48;
                                                          0;
                                                        Score 16.8; DB 17
Pred. No. 4.7e+02;
0; Mismatches 2
                                                                                  DB 17;
                                                                                    Length
                                                          Indels
                                                                                       639;
                                                          0;
                                                          Gaps
                                                           0
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Search completed: July 8, 2003, 05:51:22 Job time: 170.879 secs

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VERSION
KEYWORDS
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AU037723
                                  BASE COUNT
ORIGIN
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   Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 bp
AU037723 Dictyostelium discoideum
discoideum cDNA clone SSE216, mRNA
AU037723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ب
                                                                                                                                                                                                                                                                                                                                                                       Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                             PROJECT = 'Dictyostelium discoideum
                                                                                                                                                                                                                                                                            Institute of Biological Sciences University of Tsukuba
                                                                                                                                                                                                                                                                                                                                           DNA Res. 5 (6), 335-340 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
1 (bases 1 to 451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum.
                                                                                                                                                                                                                                                                                                            Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                              development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTATATCTACTTTCCAAAC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: M13uni primer for 3'end
                                                   170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                             Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XhoI; mRNA was made from roots of spring barley variety 'Barke', a high quality malting variety. Roots were grown for two days on filter paper at room temperature Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp"
                                                                                                                                                                                                              hideko@biol.tsukuba.ac
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                                                                            /db_xref="taxon:44689"
/clone="SSE216"
/clone=lib="pictyostelium discoideum
                                                 /dev_stage="slug"
44 c 82
                                                                                                                              /organism="Dictyostelium
/strain="AX4"
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="HW04G13u"
/clone_type="roots"
/tissue_type="roots"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hordeum vulgare"
/cultivar="Barke"
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90.0%;
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Pred. No. 3.7e+02;
   Score 16
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SS (H.Urushihara)
A sequence.
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Length 451;
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                                                                                (H.Urushihara)"
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Dictyostelium
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BQ874972
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SOURCE
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VERSION
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Best Local :
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                 AUTHORS
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 Damme, M.,
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Best Local Similarity Matches 18; Conserv
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                                                          Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                      BQ874972
QGI6M15.yg.ab1 QG_ABCDI
QGI6M15, mRNA sequence.
BQ874972
                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TATATCTACATTCGAAACGA 22
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Dictyostelium discoideum
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                  1 (bases 1 to 599)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-1-1 Tennoudai, Ts
Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                         Lactuca sativa
                                                                                                                                                                                                                  BQ874972.1 GI:22261532
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1 (bases 1 to 452)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hideko@biol.tsukuba.ac.jp
T = 'Dictyostelium discoideum
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Dictyostelium discoideum"
/strain="XX4"
/db_xref="faxon:44689"
/clone="SSE272"
/clone="Ib="Dictyostelium discoideum
/dev_stage="slug"
45 c 82 g 155 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsukuba, Ibaraki 305-8572, Japan
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Pred. No. 4.2e+02;
0; Mismatches 2;
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0; Mismatches 2;
Lavelle,D.,
                                                                                                                                                                                                                                                                               599 bp mRNA linear EST lettuce salinas Lactuca sativa
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2;
Chevalier, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 452;
                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS
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Rieseberg,L.,
egle,J., Ellison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 29-MAR-19
Dictyostelium
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                                                                                                                                                                                                                                                                                 cDNA clone
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Ziegle, J.,

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RESULT 10
BB310076/c
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AUTHORS
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BB310076
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Fax: oliver seedsc.riken.go.jp,
Email: genome-resedsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Katsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigama, T., Miki, R., Watanaba, S., Shibata, Y., Susuki, H., Tagawa, A., Sahashi, F., Tominaga, N., Toya, S., Sato, K., Shibata, Y., Susuki, H., Szuki, H., Szuki
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                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 204)
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/db_xref="taxon:44689"
/clone="ddc35g24"
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Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
Carninci,P. and Hayashizaki,Y.
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                                            Triticeae; Hordeum.

1 (bases 1 to 324)
Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
                                                                                                                                                                                                                                                                  AL501502 324 bp mF
AL501502 Hordeum vulgare Barke roots
HW04613u 3', mRNA sequence.
AL501502
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-
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/dev_stage="adult"
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/db_xref="taxon:10090"
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90.0%;
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                                        19;
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
 1 CGTATATCTACATTCGAAACGA 22
                                                                                                                                                                                                                                                                                                                                            Whole genome shotgun sequencing Unpublished (2001) Other_GSSs: BOHQB09TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGTATATCTACATTCGAAACGA 22
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19; Conser
                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Tel: 301-838-3523
                                                                                                                                                                                                                                                                                                                                 Contact: Chris Town
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                                                                                                    /clone_lib="BOHQ"
/note="Vector: pHOS1;
genomic DNA inserted :
a 203 c 180 g
                                                                                                                                                    /organism="Brassica oleracea"
/strath="TO1000H3"
/db_xref="taxon:3712"
/clone="BOHQ309"
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T9J4"
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86.4%;
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Pred. No. 2.9e
0; Mismatches
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                                                  Score 17.2;
Pred. No. 3.
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                                                                                                     into pHOS1
                                                                                                                                                                                                                                                       provided
                                                                                                                Site_1: BstXI; 2-3 kb sheared into pHOS1 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                       of Brassica
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                                                ; DB 17;
}.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υ<sub>υ</sub>
2.9e+02;
3;
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                                                                                                                                                                                                                                                                                                                                                                                   and Fraser, C.M.
                                                                                                                                                                                                                                                       Λq
                                                                                                               using
                                                                                                                                                                                                                                                                                                      20850, USA
                                                                                                                                                                                                                                                       Tom Osborn
                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   segref@genoscope.cns.fr
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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BJ156899
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AUTHORS
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                                                                                                                                                                                                                              17;
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                                                                         discoideum
BJ379738
                                                              вJ379738.1
                                                                                                                                                                                                                                         Similarity
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Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript(KS), that
was in vivo excised from a modified IPS phage vector (Mo bi Tec,
Germany). 5' end of the cDNA that was digested with XhoI was
ligated to SalI site of the vector and the 3' end including polyA
tail was ligated to BamHI site of the vector. cDNA instert could k
amplified with conventional T7 and T3 primers. This full-length
cDNA library was generated basically according to the method
described in The Plant J 15, 707-720 (1998) Seki M. et al.
Protonemata were blended by the POLYTRON, and then cultivated on
the BCDATG medium for 13-14 days under the continuous light.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ156899 full length cDNA library, gametophores Physcomitrella patens 5', mRNA sequence.
BJ156899
                                                                                                                                                                                                 BJ379738 136 bp mRNA line
BJ379738 Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 587)
Fujita,T., Shin i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyam
                                             Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plants genome
Unpublished (2002)
                  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                        Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comparison of the moss
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Carninci,P., Hayashizaki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="pph2i18"
/clone_lib="full length cDNA library, chloronemata and young gametophores"
/tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
a 132 c 202 g 127 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Physcomitrella/db_xref="taxon:145481"
                                                                                                                                                                            CDNA
                                                                                                                           GI:19289121
to 136)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%;
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Pred. No.
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Shinozaki, K.,
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3.6e+02;
thes 0;
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AUTHORS
TITLE
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BH582702
20
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ORIGIN
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Best Local Similarity
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Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; Brassica.

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                               18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                       Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
BH582702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOGTC24TR BOGT Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH582702.1
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris Town
                                                                                                                                                                                                                                                                                               DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 791)
                                                                                                           226
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R.Site 2
                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tracking errors.
                                                                                                                                                                                                                                                                 sheared ends.
                                                                                                                                                                                                                                                                                                               cdtown@tigr.org
                                                                                                           þ
                                                                                                        /clone_lib="BOGT"
/note="Vector: pHoS1; Site_1: BstXI; 2-3
genomic DNA inserted into pHoS1 using Bst
209 c 167 g 189 t
                                                                                                                                                                    /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGTC24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/d5 c 473 g 576 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="PTB-099107.R"
/sex="male"
                                                                                                                                                                                                                                                 location/Qualifiers
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94.78;
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                           Score 17.4; DB 1/,
Pred. No. 2.5e+02;
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132 others
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BOGTC24, 1
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BstXI linkers'
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                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Other_GSSs: T23P5TFB
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 ATATCTACATTCGAAACCA 89
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                                                                                                                                                                                                                                                                                                                                           l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High
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1 (bases 1 to 203)

Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B96258
T23P5TRB
                          Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                      Arabidopsis thaliana
TAMU library from st:
                                                                                                                                       survey sequence.
AL092245
                                                                                                                                                                                                       CNS00VG7
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Seg primer: M13 Reverse
Class: BAC ends
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 Salanoubat, M., Choisne, N.,
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/sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1:
/ Produced by Rod Wing"
/ 42 c 30 g 60 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3702"
/clone="T23P5"
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/strain="Columbia"
                                                                                                                          GI:5293399
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86.4%;
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                   602149264F2 NIH_MGC_62 Homo
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                                                                                     BF978743.1
                    Homo sapiens
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Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carningi, P. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared and sequenced in Mouse Genome Encyclopédia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified pBluescript KS(+) after bulk excision from Lambda
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/clone="A630008P18"
/clone_lib="RIKEN full
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/dev_stage="3 days neonate"
/lab_host="DH10B"
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                                                                               Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted ' ' ' '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1970 bp DNA Pan troglodytes DNA, clone: PTB-099107.R, AG097750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1179 row: o column: 16
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Sushiro-chou Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
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Pan troglodytes
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High quality sequence stop: 384.
Location/Qualifiers
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Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                        Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/lab_host="DH1OB (TI phage resistant)"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGTGCGACATG-dT(30)BN-3'
sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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270 c 189 g 150 t
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/clone_lib="NIH_MGC_62"
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Compugen Ltd
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Contact:
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Yoshihide Hayashizaki
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ALIGNMENTS

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Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus CE 1 (bases 1 to 213) CE 1 (bases 1 to 213) RS Konno, H. Aizawa, K. Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Togawa, A., Shiraki, T., Tominaga, N., Toya, T., Tsunoda, Y., Wattahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Konno, H., et al.) BB228117 213 bp mRNA linear EST 03-BB228117 RIKEN full-length enriched, 3 days meonate thymus musculus cDNA clone A630008P18 3' similar to D85189 Rattus norvegicus mRNA for Acyl-CoA synthetase, mRNA sequence BB228117 BB228117.1 GI:8898762 EST 03-JUL-2000

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RESULT 15
ABQ38893/c
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                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-cpG-3', present in a cytosine (c) particular cytosine in a motif 5'-cpG-3', present in a cytosine (c) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the contained on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the method for determining the degree of cytosine methylation described in the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                       Matches
        Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
                                                                            Oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-2000; 2000DE-1043826
05-SEP-2000; 2000DE-1044543
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                                                                                                                                                                         ABQ38893 standard;
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85.7%;
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Pred.
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..3e+02;
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148 CGTATATTTTAATTCGAAACG 1 CGTATATCTACATTCGAAACG Query Match
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Matches 18

Similarity

73.6%;

Score 16.2; Pred. No. 1

.3e+02

DB 24; Length 598;

18;

Conservative

0,

Mismatches

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Gaps

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Search completed: July Job time: 25.949 secs

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2003, 03:11:15

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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CT he amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers can the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders cof the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the method for determining the degree of cytosine methylation described in the invention.
Sequence 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12;
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05-SEP-2000; 2000DE-1044543
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                                                                            disclosure of the invention.
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       BP;
       261
   A; 105 Ċ;
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       other;
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12-JUL-2002

(first entry)

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RESULT 13
ABQ43723
ID ABQ43
XX ABQ43
XX ABQ43
XX ABQ43
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                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpc-3', present in a cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the method and status of many C residues to be determined simultaneously.

Comethylation status of many C residues to be determined simultaneously.

Comethylation status of many C residues to be determined simultaneously.
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Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
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05-SEP-2000; 2000DE-1044543
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18; Conserv
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Pred. No. 1
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RESULT 14
ABQ38892
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XXEX DXXXX
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gastrointestinal; respiratory system; single nucleotide polymorphism;
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05-SEP-2000;
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                           Oligonucleotide for detecting cytosine methylation SEQ ID NO 25483.
                                                                                                                                                                                                                                                                                                                                               Sequence 554 BP; 230 A; 168 C; 57 G; 99 T; 0 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-)
                                                                                              ABQ38892;
                                                                                                                               ABQ38892 standard; DNA; 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell differentiation; ds
                                                                                                                                                                                                                446 CGTAAATATAAATTCGAAACG
                                                                                                                                                                                                                                                                             al Similarity
18; Conserv
                                                                                                                                                                                                                                            1 CGTATATCTACATTCGAAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56pp + Sequence Listing; 56pp;
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000DE-1043826
2000DE-1044543
                                                             (first
                                                                                                                                                                                                                                                                                                73.6%;
85.7%;
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                                                                                                                               9
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                              Score 16.2; DB 24
Pred. No. 1.3e+02;
                                                                                                                                                                                                                466
                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German.
                                                                                                                                                                                                                                                                                                              DB 24;
                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                554;
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of
                                                                                                                                                                                                                                                                                Gaps
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Human; cytosine methylation; 5'-CpG-3';

uracil;

cytosine; diagnosis

0;

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RESULT 10
ABQ48138/c
ID ABQ48138
Вb
                               Qy
                                                                                                                                       This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucletides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two Classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cystems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cycosine methylation described in the disclosure of the invention.
                                                                     Matches
                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-371829/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2001; 2001WO-EP10074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide for detecting cytosine methylation SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200218632-A2
                                                                                    Local
                                                                                                                                                                        disclosure of the invention.
443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                 17; Conserv
                                4 ATATCTACATTCGAAACG 21
ATATCTACATCCGAAACG
                                                                                                                                     513 BP; 115 A; 41 C; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56pp + Sequence Listing; 56pp; German
                                                                   Conservative
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                                                                                  74.5%;
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426
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                                                                                  Score 16.4;
Pred. No. 1
                                                                 Mismatches
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                                                                                                                                     <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guetig D;
                                                                                                                                     189 T; 1
                                                                                  .le+02;
                                                                                                DB
                                                                                                24;
                                                                                                                                     other;
                                                                                                Length
                                                               Indels
                                                                                                513;
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                                                               0,
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RESULT 11 ABQ48139

ABQ43722

ABQ43722 standard; DNA;

ВP

0

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RESULT 12
ABQ43722/c
ID ABQ437
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                                                                                                                                                               Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-2001; 2001WO-EP10074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ48139 standard; DNA; 513
                                                                                       71
                                                                                                                                                                 Similarity
17; Conser
                                                                                                                                                                                                                                    513 BP; 189 A; 167 C; 41 G; 115 T; 1 other;
                                                                                                                            ATATCTACATTCGAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000DE-1043826
2000DE-1044543
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                                                                                                                                                                               74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin
                                                                                                                        21
                                                                                                                                                                             Score 16.4;
Pred. No. 1
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guetig
                                                                                                                                                                                 .1e+02
                                                                                                                                                                                               DB 24; Length
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                                                                                                                                                                                                   513;
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of
                                                                                                                                                             Gaps
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RESULT 8
ABQ29578/c
ABQ29578;
XX
ABQ29578;
XX
ABQ29578;
XX
De Oligonuclectide for detecting of drug; side effect; cancer; cent
KW drug; side effect; cancer; cent
KW gastrointestinal; respiratory s
KW MO200218632-A2.
XX
O1-SEP-2001; 2000DE-1044543.
XX
O1-SEP-2000; 2000DE-104543.
XX
O1-SEP-2000; 2000DE-104563.
XX
O1-SEP-2000; 2000DE-104563.
XX
O1-SEP-2000; 2000DE-104563.
XX
O1-SEP-2000; 2000DE-104563.
XX
O1-SEP-2000; 2000DE-104543.
XX
O1-SEP-2000; 2000DE-1044543.
XX
O1-SEP-2000; 2000DE-1043826.
XX
O1-SEP-2000; 200
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                                                                                                                                                                                            This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-Cp6-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the Classes of oligomers, the degree of methylation is calculated. The method CC is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation. The method allows the contribution status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the contribution of the invention.
Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplicons from chemically treated DNA
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                                                                                                                                                                               disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; 56pp + Sequence Listing; 56pp; German.
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18; Conser
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   Conservative
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                                                                                                                  353 A; 134 C; 306 G; 654 T; 0 other;
                         76.4%;
90.0%;
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                         Score 16.8;
Pred. No. 72;
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                                                            DB
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                                                         Length 1447;
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QΥ

TATATCTACATTCGAAACGA 22

B δÃ

1119 TATATATAAATTCGAAACGA 1138

Matches Query Match Best Local

Similarity

76.4%; 90.0%;

Score 16.8; Pred. No. 72;

Length 1447;

0;

Mismatches

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Gaps

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TATATCTACATTCGAAACGA 22 Conservative Sequence

1447

ВP;

654 A; 306

C; 134

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353 DB .. H 24; 0 other;

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ARCSULT 9
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                                                                                       This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpC-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CT he amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nuclet caid (PNA) oligoners CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue CC types and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously. CC abgulation status of many C residues to be determed simultaneously. The disclosure of the invention
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gastrointestinal; respiratory system;
SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
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                                                                            disclosure of the invention.
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RESULT 6
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                                      This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or paptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the Label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation of cell or tissue types and for investigating cell differentiation. The method allows the method for investing central progress to be determined simultaneously.

ABO13410-ABO54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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Best Local :
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05-SEP-2000; 2000DE-1044543
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522 BP;

64

A

70

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244 G;

141

1

other;

Query Match Best Local

Similarity

76.4%; 90.0%;

Score Pred.

No. 67;

DB 24; Length 522;

Sequence

522

BP;

141 A; 244 C; 70

G;

64 T;

3 other

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RESULT 7
ABQ42139
ID ABQ4
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                        CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue completed for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously. ABO13410-ABQ54121 represent genomic DNA sequences used to illustrate the CC method for determining the degree of cytosine methylation described in two
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Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
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Pred. No. 6
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RESULT 4
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Best Local
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                       Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. poinfections; particularly syphilis. They can also be used for diseases related to Borrelia infections in animals, and for diseases
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production of biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum.
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                                                                                                                      AAX20500-21243 represent polynucleotide sequences from the genome
                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                  products for the
                                                                                                                                                                                                                                                                       New isolated Treponema pallidum nucleic acids - used to develop
                                                                                                                                                                                                                                                                                                                           WPI; 1999-081273/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent
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                                                                                                                                                                          Page 673-685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US13041
                                                                                                                                                                                                                                               detection, diagnosis,
                                                                                                                                                                                                                       pallidum infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2515 A; 206 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; syphilis; Borrelia infection; animal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.2%;
86.4%;
                                                                                                                                                                     1150pp; English.
products such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.2;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the genome of Treponema pallidum.
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                                                                                                                                                                                                                       particularly syphilis
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Best Local
                                                                                                                                                                                                            protein product. The CASP8 gene has been localized to human chromosome 2933-34. The methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding functional CASP8 in cells. The cancer that is diagnosed or treated is a tumour in which a myc gene is amplified, such as a neuroblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                             part of the death inducing signaling complex (DISC) associated with the Fas receptor. CASP8 is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASP8 promoter region sequences, in particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation. Methylation PCR can be used to examine even minute amounts of patient material to demonstrate whether the CASP8 gene expresses an mRNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Investigation of silencing of caspase-8 (CASP8) gene by methylation was analyzed using methylation-sensitive PCR analysis. Amplification of the 5' untranslated region (UTR) of the Casp8 gene was performed in reaction mixtures containing bisulfite treated DNA. Primers AAA51818-23 were designed to produce a 320 bp fragment in the upstream region of Casp8 gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA.
                                        Aggressive neuroblastoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing prognosing cancer, comprises detecting a modification of genomic comprising the CASP8 gene that results in inactivation of the general comprises the caspase of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to amplify the corresponding region of untreated genomic DNA. Controls without DNA were also performed. CASP8, a cysteine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 61; 107pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-452423/39
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19; Conser
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    containing an inactivated CASP8
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Pred. No. 55;
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC Investigation of silencing of caspase-8 (CASP8) gene by methylation was CC analyzed using methylation-sensitive PCR analysis. Amplification of the CS with the CS were containing bisulfite treated DNA. Primers AAA51818-23 were containing bisulfite treated DNA. Primers AAA51818-23 were containing from nucleotides +221 to +541. Wild type primers were considered to produce a 320 bp fragment in the upstream region of Casp8 controls without DNA were also performed. CASP8, a cysteine protease, is controls without DNA were also performed. CASP8, a cysteine protease, is controls without DNA were also performed. CASP8, a cysteine protease, is controls without DNA were also performed. CASP8, a cysteine protease, is controls without DNA were also performed. CASP8, a cysteine protease, is controls without DNA were also performed. CASP8, a cysteine protease, is controls without DNA were also performed. CASP8, a cysteine protease, is controls a suppressor gene. The CASP8 promoter region sequences, in control to the destination of the general waterion of the caspa promoter region sequences, in control waterion, control manual control control
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Best Local S
Matches 22
                                  WPI; 2001-656860/75
                                                                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                               pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster expressed polynucleotide SEQ ID NO 26078
                 P-PSDB; ABB66429
                                                                     Venter
                                                                                                                                                                                                                                                                         WO200171042-A2
                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                   Drosophila;
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                                                                   Adams M,
                                                                                                                                           2000US-191637P
2000US-0614150
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RESULT 3
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The inventi useful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL18175) and the encoded proteins (ABB5737-ABB72072).
                                                                                                                                                                                                                15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel interactions – \,
                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour suppressor cancer; tumour; CpG dinu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                            analysing
                                                                                           genes
                                                                                                        Fragments
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                                                                                                                                                                                                                                                                                                                           W0200168912-A2
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                                                                                                                                                                              EPIGENOMICS
                                             SEQ
                                                                                                                                                      Piepenbrock
                                                                               of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
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; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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90.5%;
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de; single-nucleotide polymorphism;
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The invention relates to a nucleic acid comprising a sequence of bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and

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Run
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                SUMMARIES
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2257.229 Million cell updates/sec
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AAA51819 ABL10532 AAS46501 AAX51821 ABQ42138 ABQ42139 ABQ29578 ABQ29579

Antisense primer f Drosophila melanog Tumour suppressor Polynucleotide seq Antisense primer f Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo

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prognosing cancer, comprises detecting a modification of genomic DNA

25 522 522 1447 1447

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Match Length DB

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Description

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Search completed: July 8, 2003, 04:02:41 Job time: 83.3011 secs
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EKQAGPTRPGNYWYDYRAGFFWGVLGSHCLGILPPFIEELNYPMFENCAGGTTRVFVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="F11C10.4; predicted by genefinder" complement(join(<9088. .9392,9441. :>1052:/gene="At2g46350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(6278. .6469,6630.
7253. .7399,7602. .8483))
//gene="At2946340"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<6278. .6469,6630. .6689,6777.
7253. .7399,7602. .>8483))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MASRNSVTGFALFSFVFAVILSLAGAQSLAPAPAPTSDGTSIDQ GIAYLLMVVALVLTYLIHPLDASSSYSFF" complement(3425...3473)  
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/rpt_famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="F11010.2; supported by cDNA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="overlap with BAC clone T3F17 (AC005397:1. .7273)."
complement(2249. .2960)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVGLSVLDGYIACGSETNEVYSYYKSLPMPMTSYKFGSVDPISGNEYFDDNGQFVSSV
CWRKKSNMLVAANSTGNMKLLKLV"
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SVKLWS I NEKRSLGT IWSPANVCCVQFSSY SNHLLAFGSADYKVYCYDLRYVKTPWCT
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TLKDRDRCSENQNENQDMSTKGKSSDQLEVFFEGLCKFARYSKFETCGTIRSGDLLNS
ASVVCSLSFDPDEEHIAAAGISKKIKIFDFNAFMNESVGVHYPLVEMVNKSKLSCVCW
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/gene="At2g46330"
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                                                                                                                                                                   ETPPEFVSDQDLGSKEKKLDISKSPTPHDVLPLKSSPKGNGMYSHGDGNHSKSSIGIS
LREFLRSSYAKREKRHGLCLFRQLVELVDSAHSKRLFLLDLRFSLFTLVPSKKLRYIG
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                                                                                                                                                                                                                                                                 /translation="MPVMERVAEETVATNNIOLKARVDDVPCNKLDARHNDMVIQSETANSDCPGSSAHRNVDLTKPPPPEEAAGAKLSVEELTLGNYRIVQGSNNTNVDDSPRAGK
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NLEAFSERLRAAGENSIMNAPALISEGVQMKTPVSSNFSQLLLKRAMKGKGVVGKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(9088. .9392,9441. .10527))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At2946350"
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10966. .10990
                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAGHEKAVSYVKFMDSETIVSASTDNSLKLWNLNKTNSSGLSPGACSLTYKGHTNQKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEISELLLHFLSSLEVQKKKKASKLLQDIQTLEDDIKEAERRYSSNVSLVRSHGAIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At2946340"
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/on]tivar="Columbia"
                                                                                                    FEVWTNTQFYCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative_photomorphogenesis repressor_protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(GAA)n"
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                                                                                                                                       DSCELQQQDYIKNLSVSSVSRKQSMSTWLEEQWYTCPEEINGEDIGEKSNIYALGVLL
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SRKCKTIGALELRVVAKGTFRKIQEHFLGLGSSAGQEKMPRCVKPSNAKVLQILCENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(17871: .17892)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_
14702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(GAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical
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join(23083. .2320)
                                                                                                                                                     join(<23083. .23203,23417. )5505. .>25732)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At2g46360"
[2213. .12506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="F11C10.
                                                                                                                                                                                                                                     /gene="At2g46380"
/note="F11C10.7; |
                                                                                                                                                                                                                                                                                                                                       NKKKMEDESEWWNECCKNLEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Fl1C10.29; supported by full length cDNA: Ceres:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="At2g46375"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="At2g46370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21664. .22035
'gene="At2g46375"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="At2g46375"
!1664. .22035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1570.
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ement(1707)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _family="(TA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .20199)
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.>12506
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                                                                                                           23203,23417.
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                                                                                                        .24145,24203. .25262,25346. .25406
                                                                                                                                                                                                             by genefinder"
.24145,24203.
                                                                                                                                                                                                             .25262,25346.
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PIOCESH

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complement(15830) .17530)
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/codon_start=1
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/gene="At2g46505"
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<21510. .>24428
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complement(18392. .18
/rpt_family="AT_rich"
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GSYVAASSNPSTNTQOEKSESCTEKRPVSLLAGAGIVSVVDLEKRPKRGRKPANGREE
PLNHVEAERQRREKLNQRFYALRSVVPNISKMDKASLLGDAISYIKELQEKVKIMDE
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MEAKLSLAEDTMFHTFVIKSNNGSDPLTKEKLIAAFYPETSSTQPPLPSSSSQVSGDI
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/gene="At2g46505"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative cellular apoptosis susceptibility
protein"
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21510. .24428
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VRSYNHNNGAEEETWQDMRKRYLGKLHRLFGGSDEDNYALSKYTAFEIFFLASMY
FFRHHGEGGPGRCYSSGKHYWLSDAVUSSEDYCFRSFMAKSAGIRTIYMYDTDAGVE
LGSYWSLFENIGLYKSVQALFMRRYTQPVMYTSNTNMTGGIHKLFGQDLSGAHAYPKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative bHLH transcription factor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At2g46520"
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FEATURES
                                                                                                                                                                                                  Direct Submission

Submitted (27-FEB-2002) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org

Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org

On Apr 18, 2002 this sequence version replaced gi:6598573.

On Oct 8, 1997 this sequence version replaced gi:2443866.

We have determined that YAC YUP8H12 is chimaeric, and is comprised of two distinct genomic EcoRI fragments from chromosome I. This
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3 (bases 1 to 95214)
Town, C.D. and Kaul, S.
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1 (bases 1 to 95214)

1 (bases 1 to 95214)

1 (bases 1 to 95214)

1 (bases 1 to 95214)
                       at the bottom of the right arm of the chromosome between and m532 markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barnstead, M.E., Mason, T.M., Bowman, C.L., Ronning, C.M., Benito, M.-I., Carrera, A.J., Creasy, T.H., Buell, C.R., Town, C.D., Nierman, W.C., Fraser, C.M. and Venter, J.C.
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AC006526.8 GI:20197817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                          (right end) to position 181918 of our previous submission YUP8H12 accession number AC000098.
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microsatellite repeat region (clone 74A)#Rf:ATR0046|X93607
74A"
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microsatellite repeat region (clone 74A)#Rf:ATR0046|x93607
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nicrosatellite repeat region (clone 74A)#Rf:ATR0046|X93607
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microsatellite repeat region (clone 74A)#Rf:ATR0046|X93607
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Pred. No. 5.4e+02;
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ORGANISM
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VERSION
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                                                                                                                    Direct Submission
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research,
Medical Center Dr, Rockville, MD 20850, USA, cdtownstigr.or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 84825)
1 (bases 1 to 84825)
1 Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E.,
Bennito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D.,
Nierman,W.C., Fraser,C.M. and Venter,J.C.
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                                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-2000) The Institute for Medical Center Dr., Rockville, MD 20850, U 3 (bases 1 to 84825)
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HTG.
                                                                                                                                                                                                                                                                                           Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                     Center Dr, Rockville, 18, 2002 this sequence Location/Qualifiers
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CILYQMVYGRTPFADYKTFWAKEKVITDPNHEITYNQLSNPWLIDLMKKCLAWDRNQR
WRIPELLQHPFLAPPIPHEPQVKTIKLESLIAESCGSDDKANSMISQLEQLLSNPAP
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EAPVGSSIYGSDQANARLPEELHTSVSSQKSBKHEKASSKQPSAPKRNYDPDL
ETKVNGKLYQRLGKIGSGGSEVHKVISSDCTIYALKKIKLKGRDYATAXGFQQEIGY
LKKLKGKTNIIQDIDYEVTDKTLLQEVLNGTMSNKDGRVKEDGFIYMVLEYGEIDLAH
MLSQKWREIEGSDRTIDENWLRFYWQQILQAVNTIHEERIVHSDLKPANFLLVRGFLK
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LIGGESLRFICRHSKRGDVHSPGKPLGQIHLKVSSIGQSISDGKRFTVFTGTKSLHLR
AATSEDRASWIEALKAVKETFPRMSNEELMASTTNVSVSTDKLRQRLMEEEVDETIIK
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27895. .31218
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/codon of:
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join(21802. .22
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[Arabidopsis thaliana]; Pfam HMM
homology) domain"
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/protein_id="AAG51621.1
/db_xref="GI:12323289"
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/organism="Arabidopsis thaliana"
/cultivar="Columbia"
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Pred. No. 5.4e+02;
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w hit: PH (pleckstri
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complement(11207...13602)
/gene="At2946500"
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/gene="ht2946480" complement()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /wuce="overlap with BAC clone F11C10 (AC006526:59064, .95416)." complement(1047, .3029) /gene="At246480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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RSESVESGSENLKYRYPKYMSMLNHLRFYIPRIFPKLEKILFVDDDVVVQKDLTPLÆS
IDLKGKVNENFDPKFCGWAYGMNIFDLKEWKKNNITETYHFWQNLNENRTLÆKLGTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="(CAT)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2074. .2431,2503. .2828,2916. .3029))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(11384. .11764,11858. .13177))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGLITFYNLTQPLQRKWHLLGLGYDKGIDVKKIERSAVIHYNGHMKPWTEMGISKYQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YWTKYTNEDHPY IFTCRLEE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="overlap with BAC clone F11C10
/AC006526:59064 95214\"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="At2g46490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ′gene="
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      At2g46490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .4517)
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COMMENT
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                             gene
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                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of GlimmerM, see Mihaela Pertea,
http://www.ttgr.org/softlab/glimmerm.htm/glimmerm.html, and
GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
mpertea@tigr.org), searches of the complete sequence against a
peptide database and the plant EST database at TIGR
(http://www.tigr.org/tdb/tgi.shtml), Annotated genes are named to
indicate the level of evidence for their annotation. Genes with
similarity to other proteins are named after the database hits.
Genes without significant peptide similarity but with EST
similarity are named as unknown proteins. Genes without protein
or EST similarity, that are predicted by more than two gene
prediction programs over most of their length are annotated as
hypothetical proteins. Genes encoding tRNAs are predicted by
tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
Simple repeats are identified by repeatmasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology/gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JAN-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or On Jan 19, 2001 this sequence version replaced gi:12280880. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The orientation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone T32E8 is orientation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1. .3320)
complement(1. .3320)
fote="%inilar to ribonuclease II RNB family protein
GB:GAB16367 [Schizosaccharomyces pombe]; Pfam HMM hit:
VacB and RNase II family 3'-5' exoribonucleases"
complement(join(<1. .69,154. .2280,2381. .2449,2524. .26'6. .3055,3215. .>3320))
Gene="%initar family 3'-5' exoribonucleases"
                                                                                                                                                                                                                                                                                                    WPKMKFFVTESAAKPEGTNSPPEKDKKARQKNGIDVVEGFEDGFSKNKSSVIGKGAK
NGVTPSSPPSLDSCLGSFCEOKONCSAVDKLCGILSSFPHKRFFGQVVAVVEKSLVRD
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SIVGLLDVKGWIHYKESDPKRCKSPLSLSDDESVQLMAPDRFPKLIVPFHVLPGSIR
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SDFSPGSLTSLPRVPWEVPEEPCALDTEAFRSTSVVLMQRKISMLFPLLSENVGSLSPGADR
FRVGVHLADVSYFVLPETALDTEAFRSTSVVLMQRKISMLFPLLSENVGSLSPGADR
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LEKGEAFKALFRVNAHNRNEAYCKIDGYPTDILINGNVCQSRAVEGDTYVIKLDPLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(<1. .69,154.
2676. .3055,3215. .3320))
/gene="T32E8.1"</pre>
complement(8589. .10716)
/gene="T32E8.2"
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LYTHFTSPLRRYPDIVVHRALAAALEAEELYSKQKQTAIDEGRSCFTGIHFNKDAAES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Columbia
                                                              /note="overlap with BAC clone
[AC010704:103165. .103353]."
                                                                                                                                                                                                         IEGKEALSVAALKHGVPSTEILSDVAAYCNERKLAARKVRDACDKLYTWFVLKQKEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .82454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2280,2381.
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ed gi:12280880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2449,2524.
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join(14054.../gene="T32E8...
join(14107...
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LKCSASGKPFASLAEFTLAALDFVDSLVDGENLPMSVFMNOKGNCSVAGCYADLRF
HCPQELAVKSNGKVISCRSACDVFDRDEYCCRGVYGNPVVCQPTYYSKIFKQACPTAY
SYAYDDPTSIKTCTAADJYLISFCSSRFYLFTFLTTSHDYFNYDSNQVSFILDHDFYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vtranslation="MAAEKIETVVAGNYLEMEREEENISGNKKSSTKTKLSNFFWHGG
SVYDAARSCASNOVAOVLLTLPYSFSOLGAMSGLIFQLFYGLMGSWTAYLISVLFVEY
RTRKEREKEDEREDERNHVIGWFEVLDGLLGKHWRNLGLIFNCTFLLFGSVIGLIACASNIY
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AEDVKHSGPTTMVLYFTGATNILYTFGGHAVTVEIMHAMWKPOXFKAIYLLATIYVLT
LTLPSASAVYWAAFGDKLLTHSNALSLLFKTGFROTAVILMLTHOFTFGFASTPLYFV
WEKLIGVHETKSMFKRAMKRLPVVVPIWFLAIIFPFFGFBINSAVGSLLVSETVYITJAHMLTFAPAPSRENAVERPPRVVGGWMGTYCINIFVVWVFVVGFGFGGWASMVNFV
ROLDFFGLFTKOYQCPPHKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to AUX1 (regulator of root gravitropism, putative permease) GB:CAA67308 [Arabidopsis thaliana]" complement(join(<8589. .8783,9000. .9465,9555. .9652,9753. .9936,10020. .10132,10236. .10421,10504. .>10716))
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join(<18583. .18916,19056. .19948,20068. .20268,20382. .20543,20662. .21388)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(8589. .8783,9000. .9465,9555. .9652,
9753. .9936,10020. .10132,10236. .10421,10504. .10674))
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[Caenorhabditis elegans]"
join(14054. .14174,14251. .14348,14779. .14811.1
/gene="T3258.4"
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//gine="T32E8.3"
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join(12104. .
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[Arabidopsis thaliana]; Pfam HMM hit: Thaumatin fami.
join(<12104. ...12179,12505. .12628,12704. .>13574)
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/protein_id="AAG51630.1"
/db_xref="GI:12323298"
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/gene="T32E8.5"
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519.1"
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/protein_id="AAC65057.1"
/db_xref="G:332320"
/tanslation="MADVHYVILVGRILTRDAELKYTSAGGALCRESVAINRRRKSGDD
/translation="MADVHYVILVGRILTRDAELKYTSAGGALCRESVAINRRRKSGDD
WYEEVNRFDIVLMGRQGEVISQYLIKGKQVAVEGELRQSRWEQEGQSRSKVEISATNV
QLLGSVILGGAARAEDGEFSSSRVAAESTAGRVRGTSSDSRSPTGDILGEKRGLDATSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="T. pallidum predicted coding region TP0064"
/protein_id="AAC65064.1"
/db_xref="G1:332327"
/db_xref="G1:332327"
/db_xref="G1:332327"
/translation="MLPTAQRRLRGYIRACAPYGRRGEEPVRRRCAFLCARVGHVCVG
RSVVQNFVFQDNIYHLARSIDVLYEGLQLULDECLYAEKVVYDVRFFDHÄLQKLCAHI
DRQSHFPDYLPILHCLFSCGARFLULLNFLIHRASPVTAQVEFTRMLPFIEKRHSALH
DRLARSIQEVDTSADASHVVSQDEIDELLEH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MRTYELMAVFSAHEDLFLQGSTAVRALLQENDAVIAREDHIGER ELAYPLKKQKRGRYLLFIVQCEPGKVRELDHKLRLRHDLLTHLFVRVDS" 3555. .4130
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/gene="TP0063"
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/protein_id="AAC65056.1"
/db_xreff="G1:3322319"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="maedhpsydldThlsspreseesapkknrofyrkkycrfcTokl
LADYKDPDTLRRFITERGKILPRRITGTCAKHORRVALEVKRSRAVALLPFVLTE"
                                                                                                                                                                                                                             /translation="MLKNHVLRCPDGPIRPAMDRMRESLFAILGDMRGCSFLDLFAGS
GVCGLEAYSRGAYPVVFVEWNVRSFSVLLQNVQVALCRLECRCMAVERYIARARTLFH
FVYLDPPFPYRFHAELLQRLSRASLCREGSVVMVHRPREKKLADKIDSLVRTDQRVYG
                                                                                                                                                                                                                                                                                                                                                                                              /gene="TP0065"
/note="similar to GP:1694865 percent identity: 36.11;
identified by sequence similarity; putative"
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4204. .4791
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/protein_id="AAC65058.1"
/db_xref="GI:3322321"
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4775. .5089
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/protein_id="AAC65059.1"
/db_xref="GI:3322322"
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/transl_table*11
/product="T. pallidum predicted coding region TP0066"
/protein_id="AAC65065.1"
                                                                                   /note="hypothetical
putative"
                                                                                                                        /gene="TP0066"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
Medical Center Dr. Rockville,
3 (bases 1 to 82454)
Town,C.D. and Kaul,S.
Direct Submission
                                                                                                                                                                  Lin, X. and Kaul, S.
Direct Submission
Submitted (21-OCT-1999)
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DGYAFILKVNDLERAESBEGKILOIEADNINALVGLGDAARKERAKVQEASDYYTRCLQH
YPRNSYALFGLADCYKNMRRYVKAVEVWQQYYEADLAVLTRMADAYRKIHDFQNS
RNLYSQVIALDEHNSYALIGLAHLHYDFKKYREALIYWKKLLECAEHSVDIRVLTSIG
NCYRKMKLFSQGLPYFGBALKRDPGNFYGFFGMADCYRGMNMQERSIQYWEKILEKDT
QNRVILTRIADAYRHIGEYEKAHQTYKRALDIDYDAYATLGLAVLCKLQGRYEEAVVS
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/translation="MQRVLESDTPYFVKGIQRPVSTLSDRDRALLNRRGNAYLNEGKL
QEAARVFITTGYHDGLTRIGDVYMRKADVLTALRFYYFARNEQKMRPIVSALSVLIRC
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5077. .6258
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/product="conserved hypothetical
/protein_id="AAC65061.1"
/db_xref="GI:3322324"
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/db_xref="GI:3322323"
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identified by sequence
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86.4%;
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Pred. No. 5.7e+02;
                                                                                                                                                                           The Institute for Genomic Research,
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50.1"
                                                                                                                                        MD 20850, USA, xlin@tigr.org
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                                                        Fraser,C.M., Norris,S.J., Weinstock,G.M., White,O., Sutton,G.G., Dodson,R., Gwinn,M., Hickey,E.K., Clayton,R., Ketchum,K.A., Sodergren,E., Hardham,J.M., McC., Salzberg,S., Peterson,J.Khalak,H., Richardson,D., Howell,J.K., Chidambaram,M., Utterback,T., McDonald,L., Artiach,P., Bowman,C., Cotton,M.D., Venter,J.C. et al.
                                                                                                                                                                                                                                                                                Treponema pallidum section AEO01191 AEO00520 AEO01191.1 GI:3322316
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  spirochete
Science 28
                                     Complete genome sequence of Treponema pallidum,
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Treponema pallidum
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
1 (bases 1 to 11101)
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SPNYMQIFLLLISPESWKRSGNVPALVRLLQAFLQKAPHEVTQDIRLSQVLGIFEKLV
ASPSTDEOGFYLLNT IIELLDYSVLAPYMKGVMSALFTRYQNKKTVKFQKSLVIFMSL
ELVKHGQAYLVEEMNTVQPNITAIVEHEWIPHLKLINGSMEVKLITAVAATRLICETP
ALLDPSAAKLMGKMLDSIVTLVSRPEQERVLDEPEMPBISENVGYTAAFVKLHNAGKK
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
/note="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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ROATEKLLKNLIPDLVNTIETRYRNOSDLVGIATGLTALDNLTGGFQNSELIVIGARP
SMGKTALAMTMASNIALTRGRIPTAFFSLEMSNLLLMRRLICABESGVSATNLRRGLIQL
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NFFAPRYEQFAAISQSLKSLARELDIPTVALSQVGRPAEGSANUADIRGSGAIEQDA
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ARFKQRQQDIEMRKSLKRQDAANLKARLEAQPYVIAMPAGTNGKLYGAVTSHTVAEQL
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                  complement(2177.
/gene="TP0061"
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/gene="TP0060"
                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1601. .2071)
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              /codon_start=1
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19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Salk, Stanford, PGEC (SSP) Consortium members carried out sequencing and annotation of the RAFL CDNAs: Southwick,A., Nguyen,M., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamadda,K., Ecker,J., Theologis,A. and Davis,R.W.
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e-mail
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY093111 2438 bp mRNA linear PLN 21-APR-20 Arabidopsis thaliana putative protein (At3g56140) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (27-MAR-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rossidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equally to this work. Shinozaki, K. (RIKEN GSC) a (SSP/Stanford) contributed equally to this work
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southwick, A., Karlin-Neumann, G.,
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                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
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/note="This clone is in pBluesc:
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AESAAPPPPPATTTPSPPPPVNKEETTTSRTYDATATGEPMAMGKDKKKVWEKLLNAR
VVYLGEAEQVPTKDDKELELETVRNLRKRCVESERQTSVALEAFPLDLQDQLNQYMDK
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/protein_id="AAM13110.1"
/db_xref="GI:20260424"
/tzanslation="MXLTTNDLFASQPLFHCPCSSSSRPRRRRFYGLHFPINLTSEKN
                                                                                                                                                                                                                                                                                                                                                                   ecotype:
                                                                                                                                                                                                                                                                                /gene="At3g56140"
/note="F18021.100"
RMDGETLKSYVTHWPAQRWQEYEPLLSYCRDNSVRLIACGTPLKVLRTVQAEGIRGLS
                                                                                                                                                                                                           /codon_start=1
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90.5%;
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ls work. Shinozaki,K. (RIK)
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Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                           pBluescript
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Direct Submission
Submitted (05-JAN-2001) Haasen D.
Submitted (05-JAN-2001) Haasen D.
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Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; eurosids II; Brassicales; Brassicacea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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QVILQAVADGGGTGLLLVVTGASHVEYGSRGTGLFARISRKFFKKNQVVVLLDBERQF
LRREGETPVADFLWYSAARPCSRNCFDRAEIARKMNAVAFRRDALPFDIQNGLDLELV
SPEVLQNLFDLEQYPLISAELTQRFQGFRERLLADPKFLMRLAIBEAISTTTLLAQYE
KRKENFFEEIDYVITDTVRGSVVDFFTVWLPAPTLSFLSYADETTGPDSIDALRGLLG
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PELVVAEKPKRSPLLKTAMVYGGFLGTSANLRYQIIAGLIEHRLSDELSSQPLLVNAI
                  ESQRICCTIFYSLIFODLPEFFEDHNKEWMGEEKKYLSSNYALESTEEGGITLVDDLR
AAICENINHYIEKNEEEFQGFINEFASVVWTLLEDDYSKSPSRDQLATTA,KKFLTSVSI
SVHHALFAGDNVIKEICQSIVIPNVSLRVEDBEIFEMMYIEFIRDMESGDVDTRRRI
ACELLKGLATNYKTQVTEVVSLEIQRLLSSFSANPSANWKDKDCAIYLVVSLSTKKAG
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/db_xref="GI:18077710"
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                                                                                                                                                                                                                                                                                                                            /function="nuclear export receptor for importin alpha"
/note="CAS interacts with importin alpha 1-4 and with ran
from Arabidopsis thaliana"
GASVSTDLIDVQNFFANIILPELQSRDVNSFPMLKAGSLKFLTMFRSHTPKPFAMQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis t.
/variety="ecotype Col-0"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                     /evidence=experimental
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Pred. No. 6e+02;
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Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J

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FEATURES
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[alt 3]"

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                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                    source
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RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Roll, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Davison, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Dodson, K., Center, A., Carlson, J.W., Center, A., Carlson, K., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Lipe, Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Welson, C., Welson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., A., Peclon, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Saguencing of Drosophila chromosome X, region 16B-16D
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                  shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On May 12, 2001 this sequence version replaced gi:6435885. Sequence submitted by:
                                                                                                                                                                                                                                                                                                  Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                This sequence was assembled using end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                           location/Qualifiers
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Pred. No. 2.
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                                                          melanogaster'
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x, region
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5D, BAC clone
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                                                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 300994)
Ephydroidea; Drosophilae; Drosophila.

2 (chases 1 to 300994)
Ephydroidea; Drosophilae; Drosophila.

2 (chases 1 to 300994)
Exphydroidea; Drosophilae; Drosophila.

2 (chases 1 to 300994)
Exphydroidea; Drosophilae; Drosophila.

2 (chases 1 to 300994)
Exphydroidea; Drosophilae; Drosophilae
Exphydroidea; Drosophilae; Drosophilae
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AE003506 AE002593
AE003506.1 GI:7293355
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19; Conser
                                                                                 Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X.H., Zhong, F.N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M., and Venter, J.C. The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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pBACe3.6)"
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
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36053 section 23
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                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 134421: contig of 134421 bp in length
* 134322 134521: gap of 100 bp
* 134522 134521: contig of 10141 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted (02-JUN-2002) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 2, 2002 this sequence version replaced gi:18308604. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2218
Center clone name: 2005_H_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
/clone="CTD-2005H15"
/clone_lib="CITD1 Human BAC"
30377 c 29991 g 42108 t
                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                 /chromosome="15"
/map="15"
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                 100 bp
10141 bp in length
144 others
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CE 1 (bases 1 to 169856)

RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Busam, D.A., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Frise, E., Galle, R.E., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Seguencing of Drosophila chromosome X, region 16D-16F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kaim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Packleb, J.M., Park, S., Ffeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, B., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory, MS 64-121, Berkeley, CA 94720, USA on May 5, 2001 this sequence version replaced gi Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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                                                                                                                                                                                                                                                                                                               This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-OCT-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 169856)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submission
/clone="BACR01N10 (D1115)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
                                                                                             /map="16D-16F"
                                                                                                                              /organism="Drosophila melanogaster"
/Strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="X"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169856 bp
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Best Local
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                                                                                                                                                                         DE 3 (bases 1 to 132202)

SE Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boyuslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., Deartellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., Deartellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Methews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phankhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tegfaye, S., Wilson, B., Stanger, A., and Zody, M., Sembek, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Nusbaum, C., Lander, E., Ali, A., Alien, N., Anuer, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacGonald, P., Major, J., Matthews, C., MacCarthy, M., Melotim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Melotim, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Melotim, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Melotim, J., Martheys, C., Norman, C., H.
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AC129980.3 GI:22297424
HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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IN PROGRESS ***, 2 ordered
Submitted (19-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 19, 2002 this sequence version replaced gi:22213335. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 15, Unpublished
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Birren, B., Nusbaum, C.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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me 15, clone CTD-2529M12
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Pred. No. 2.7e+02;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 144662)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone CTD-2005H15

Unpublished
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Ginde,S., Gora,S., Goyecco,, Hulme,W., Iliev,I., Johnson,K. Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,K. Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Landers,T., Lehoczky,J., Levine,R., Liu,G., Macazares,R., Landers,T., Lehoczky,J., Marquis,N., Mathews,C., MacCean,C., Macdonald,P., Major,J., Marquis,N., Mathews,C., McCarthy,M., McEwan,P., McKernan,K., McDheeters,R., Meldrim,J., McCarthy,M., McEwan,P., McKernan,K., McDheeters,R., Meldrim,J., McCarthy,M., McEwan,P., McKernan,K., McDheeters,R., Meldrim,J., McCarthy,M., 
                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 144662)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collynore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, Cooke, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Bouther, J., Grand-Pierre, N., Graham, L., Grand-Pierre, N., Grand-Pierre, Grand-Pierre, Grand-Pierre, Grand-Pierre, Grand-Pierre, Grand-Pierre, Grand-Pierre, Grand-Pie
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Homo sapiens chromosome 15 clone CTD-2005H15 map 15, *** SEQUENCING
IN PROGRESS ***, 2 ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 128: contig of 128 bp in length
129 228: gap of 100 bp
229 132202: contig of 131974 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/db_xref="taxon:9606"
/chromosome="15"
/map="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CTD-2529M12"
/clone_lib="CITD2 Human BAC"
27502 c 28043 g 38577 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                 Iliev, I., Johnson, R.,
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Š 밁

SOURCE

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ORIGIN

#Match: GSS: Em:AQ531595"	(39564 ch: GSS:	4114) Em:AQ117010"	épe	/note="match: GSS: Em:AQ059372"	/note="match: GSS: Em:AQ261089"	/note="match: GSS: Em:AQ009565" 30743453	GSS	"match: GSS: Em:AQ245895" ment(28873061)	U	natches 39354	t: matches 5338597	: GSS: Em:AQ692/85"	0 0	.1877 ="match: GSS: Em:A0810603"	1431. 1896 /note="match: GSS: Em:AQ669827"	Ĭ.	note="match: GSS: Em:AQ738677"	/mote="match: GSS: Em:AQ537460" 1451223	note="match: GSS: Em:B76221" 450 2017	/note="match: GSS: Em:AQ474420"	/note="match: GSS: Em:AQ355624" 1448. 1964	/note="match: GSS: Em:AQ275646" 1447 1837	e="match: GSS: Em:AQ585548" . 1761		note="match: GSS: Em:AQ047100" 3622055	/note="match: GSS: Em:AQ901298" 12941860	note="match: GSS: Em:AQ826107" 294 2055	note="match: GSS: Em:AQ879547" 290. 1693	ംം	complement(0981442)  note="match: GSS: AQ896860"	/note="ILM3 repeat: matches 27323226 of consensus"	/note="match: GSS: Em:AQ383567" A75	note="L1M4 repeat: matches 25823669 of consensus"	
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2 1	repeat: matches 11888 of c	atches 1.	<pre>/note="LTR14A repeat: matches 1344 of co LTR14A repeat: matches 1344 of consensus</pre>	4853 of cons	es 40604853	eat: matches 2327 of cons	repeat: matches 2327	<pre>/note="L1PB1 repeat: matches 60086155 of consensus L1PB1 repeat: matches 60086155 of consensus"</pre>	natches 3477 of consens	.8082 ="MADE1 repeat: matches 34		repeat: matches 295445 o .7774	MER65A repeat: matches 299	/note="match: GSS: Em:AQ095672"	/note="match: GSS: Em:AQ052109" 65466741	GSS:	.6787	G 600 :	match: GSS: Em:AQU956/2 5686	::AQ434336 5541	GSS: EH: HQZ14003	0 0		GSS: Em: AQ344327	CCC . EH	7:000 march: 000: bm:200:000 6213. 6543 /note="match: Gss: Em.20382827"		matches 132. 428 or	5976 LTR16A repeat: matches 132	52045675 /note="match: GSS: Em:AQ712434"	51545605 /note="match: GSS: Em:AQ608022"	514/5639 /note="match: GSS: Em:AQ076436"	51473736 /note="match: GSS: Em:B60185"	מכנות

in length

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100 L

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29789 30507: contig of 7
30508 30607: gap of 10
30608 31313: contig of 7
31314 31413: gap of 10
31414 32105: contig of 6
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585 33788: gap of 100 b

785 34486: contig of 702 l

87 34586: gap of 100 b

37 35310: contig of 724 bt

1 35410: gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 36129: contig of 719 bp
30 3629: gap of 100 bp
30 3759: contig of 715 bp
45 37759: contig of 715 bp
60 37859: gap of 100 bp
60 38559: contig of 693 bp
53 38652: gap of 100 bp
53 38652: gap of 100 bp
53 38659: gap of 100 bp
53 38741: contig of 720 bp
75 39474: contig of 716 bp
76 39476: contig of 716 bp
77 39476: contig of 716 bp
78 39476: contig of 716 bp
78 39476: contig of 716 bp
78 39476: contig of 716 bp
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7 44286: gap of 10
7 44996: contig of 7
7 45096: gap of 10
7 45096: gap of 10
6 45915: gap of 10
6 45915: gap of 10
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2 28045: cont
6 28145: gap of
28868: cont
                                                     50823: ga
51512:
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23370: gap of 100 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24955:
                                                                        49910: contig of 724 bp in length 50010: gap of 100 bp 50723: contig of 713 bp in length 50823: gap of 100 bp
                                                                                                                                                                                                                                                     46631: contig of 716
46731: gap of 100 b
47449: contig of 718
47549: gap of 100 b
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                                                                                                                                                                   49186:
                                                                                                                                                                                                             48375:
                                   51612:
                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
13490: contig of 693 bp
13490: gap of
44186: com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
100 bp
18968: contig of 723 bp
18968: gap of
29688: con-
100 b
100 b
11612: contig of 689 b
11612: gap of 100 5
52318: cont
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24068: c
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26429: contig of
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25652: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27231: contig of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
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100 bp
1710 bp
                                                                                                                                                                                                                  100 bp 1
1726 bp 1
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100 bp .
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f 684 bp
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f 692 bp in length
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f 719 bj
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dq 901
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repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL Submitted (18 AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone-requests: clonerequest@sanger.ac.uk
On Jul 14, 2000 this sequence version replaced gi:8894204.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43249 GTCTATCTACATTGGAAACGA 43269
                                                                                                                                                                                                                                                Group. Further information can be tourned the fibrily www.sanger.ac.uk/HGP/Chri RP4-813B7 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For furth details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL137861 127682 bp DNA linear PRI 01-NOV-20
Human DNA sequence from clone RP4-813B7 on chromosome 1 Contains
pseudogene similar to zinc finger protein ZNF186, STSs and GSSs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GTATATCTACATTCGAAACGA 22
                                                                                                                                                                                                                                                                                                                                                                              The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 127682)
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                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                    ence is the entire Location/Qualifiers
                         /clone="RP4-813B7"
/clone_lib="RPCI-4"
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/note="Alux repeat: matches 75.

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RESULT 2
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone CTD-2010D2
                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
                                                                                                                                     Submitted (29-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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AC103875.1 GI:17149760
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Homo sapiens chromosome 11 clone CTD-2010D2 map 11, LOW-PASS
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t, A.F.A. & Green, P. (1996-1997)
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Pred. No. 2.8e+02;
0; Mismatches 2
Institute/ MIT Center for
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
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------- Project Information
Center project name: L22053
Center clone name: 2010_D_2
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1528: contig of 723 bp in length
1628: gap of 100 bp
2350: contig of 727 bp
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4797:
21768: gap of 100 bp
22487: contig of 719 bp in
22587: gap of 100 bp
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6395:
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21668: contig of 718 bp in length
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: gb_ba:*
2: gb_htg:
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Pred. No. ST the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	ACCESSION ACCUS DEFINITION
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neophera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  1 (bases 1 to 20306) Adams, M. and Venter, J.C.	AC019801.1 GI:665096 AC019801.1 GI:665096 HTG; HTGS_PHASE2. Drosophila melanogaster. Drosophila melanogaster	AC019801 20306 bp DNA linear HTG 03-JAN-2000 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces

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; ORGANISM: Aspergillus fumigatus US-10-128-714-563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 5563
LENGTH: 4048
TYPE: DNA
ORGANISM: Aspergillus fumigatus
US-10-128-714-5563
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US-10-128-714-5563/c
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                                                                                                                                                                                RESULT 14
US-10-770-333-67/c
(S-10-770-333-67/c
; Sequence 67, Application US/10270333;
publication No. US20030092124A1
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Es
TITLE REFERENCE: 10182-018-999
FILE REFERENCE: 10182-018-999
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Best Local Similarity 85.0%;
Matches 17; Conservative
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SEQ ID NO 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                 APPLICANT: Cravchik, Anibal
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
ETLE REFERENCE: CL000733CON
CURRENT APPLICATION NUMBER: US/10/270,333
CURRENT FILING DATE: 2002-10-15
CURRENT FILING DATE: 2002-10-15
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PRIOR APPLICATION NUMBER: 60/168,677
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                                                                                                                                                                                                                                                                                                                                                     ch 72.4%; 1 Similarity 85.0%; 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.2; DB 9;
Pred. No. 2.7e+02;
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Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4048;
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; ORGANISM: Drosophila
US-10-270-333-67
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US-10-224-413-3
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                                                                                                 QΥ
Search completed: July Job time: 30.6338 secs
                                                                                                                                                                                                         US-10-224-413-3
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SOFTWARE: FastSEQ for Wind
SEQ ID NO 67
LENGTH: 9249
                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ
SEQ ID NO 3
LENGTH: 42571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10224413 Publication No. US20030013167A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/175,691
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/191,638
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL001169

CURRENT APPLICATION NUMBER: US/10/224,413

CURRENT FILING DATE: 2002-08-21

PRIOR APPLICATION NUMBER: 09/810,347

PRIOR FILING DATE: 2001-03-19

RUMBER OF SEC ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 72.4%;
Local Similarity 85.0%;
hes 17; Conservative
                                                                                                                                                    Local
                                                              22240 AGGGTAATCTGAGATTGCGA 22259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 TCGGGGTGTCGGAGATTGCG 327
                                                                                                                              72.4%;
al Similarity 85.0%;
17; Conservation
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                                                                                                 2 AGGGGATTCGGAGATTGCGA 21
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                                                                                                                                                    Score 15.2; DB 9; Pred. No. 3.2e+02;
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Pred. No. 2
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                                                                                                                                       Mismatches
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                                                                                                                                                                          DB 9;
                                                                                                                                                                      Length 42571;
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                                                                                                                                       0;
                                                                                                                                     Gaps
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 192
SEQ ID NO 192
                                                                                            ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AII70752 US-09-917-800A-881
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TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-770-444-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/917,800A CURRENT FILING DATE: 2001-07-31 PRIOR APPLICATION NUMBER: US 60/22,040 PRIOR APPLICATION NUMBER: US 60/22,040 PRIOR FILING DATE: 2000-07-31 PRIOR APPLICATION NUMBER: US 60/22,880 PRIOR APPLICATION NUMBER: US 60/29,029 PRIOR APPLICATION NUMBER: US 60/290,029 PRIOR APPLICATION NUMBER: US 60/290,645 PRIOR APPLICATION NUMBER: US 60/290,645 PRIOR APPLICATION NUMBER: US 60/29,336 PRIOR APPLICATION NUMBER: US 60/29,336 PRIOR FILING DATE: 2001-05-12 PRIOR FILING DATE: 2001-05-22 PRIOR FILING DATE: 2001-05-22
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US-09-917-800A-881
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Best Local Similarity
Matches 17; Conserv
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 881
LENGTH: 721
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                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 881, Application US/09917800A
  Best Local Similarity
Matches 17; Conserva
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                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/303,459 PRIOR FILING DATE: 2001-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 44921-5038-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/297,457 PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/295,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                   LENGTH: 721
TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/298,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 TATCGGATTCGGAGATAGCG 348
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Castle, Arthur
Elashoff, Michael
Conservative
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                            72.4%;
85.0%;
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Pred. No. 2.4e+02;
                            Score 15.2;
Pred. No. 2
    Mismatches
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                          2.5e+02;
                                             DB 10;
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    Indels
                                          Length 721;
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-128-714-563/c
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 595
LENGTH: 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 563, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                    APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sabastien M
APPLICANT: Lemieux, Sabastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT ETILIG DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 TAGGGGACTCGGAGGTTGGG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TAGGGGATTCGGAGATTGCG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIZOGUCHI,
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b. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10128714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1074;
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269 AGTGGACTCGGAGATCGCGA 250

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; LOCATION: 17, 51, 166
; OTHER INFORMATION: a, t,
US-09-294-093B-1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-294-093B-1232/c
δõ
                                                                                                                         ; NAME/KEY: unsure
; LOCATION: 13, 44, 47
; OTHER INFORMATION: a,
US-09-294-093B-775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-294-093B-775/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 1232
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1232, Application US/09294093B Patent No. US20010051335A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: APPLI 21, 1998
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 775
PERL Program
SEQ ID NO 775
PERL Program
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                                         Query Match
Best Local Similarity
Matches 17; Conserv
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CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700343292H1
                                                                                                                                                                                                                                                                 LENGTH: 285
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. US20010051335A1 700343985H1
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nes 17; Conserv
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  2 AGGGGATTCGGAGATTGCGA 21
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                                           Conservative
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85.0%;
                                                            72.4%;
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Pred. No. 2
                                                            Score 15.2; DB 10;
Pred. No. 2.3e+02;
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RESULT 8
US-09-770-791-820
"~~nuence 820, Ap
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US-09-770-444-192/c
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Best Local S
Matches 17
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SEQ ID NO 820
LENGTH: 342
TYPE: DNA
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                                                                                   APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/770,791
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR FILING DATE: 2000-01-27
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                                         APPLICANT:
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Allen, Keith
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Rameaka, Joshua G.
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Hamilton, Carol M.
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Davis, Keith R.
Allen, Keith
                           Kricker, Maja
Slader, Ted
                                                      Garcia, Carlos A.
                                                                      Woessner, Jeffrey P.
Haas, William David
                                                                                                                                          Rameaka, Joshua G.
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                                                                                                 Ledford, Brooke L.
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85.0%;
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Pred. No. 2
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APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: GLYCINE METABOLISM ENZYMES
FILE REFERENCE: BB1192 US CIP
CURRENT APPLICATION NUMBER: US/09/873,880
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/363,321
PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: July 38, 1998
PRIOR FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 42
US-10-037-270-446
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Jie
                                                                                                       NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 446
LENTH: 1471
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SEQ ID NO 29
LENGTH: 1362
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                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/037,270 CURRENT FILING DATE: 2002-01-04 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR FILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                  APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids
TITLE OF INVENTION: PolyPeptides
FILE REFERENCE: 784CIP2B
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            NAME/KEY: CDS
LOCATION: (904)..(1293)
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                                                        FEATURE:
                                                                    ORGANISM: Homo sapiens
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US20020123118A1
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Wang, Zhiwei
Tillinghast, John
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Chen, Rui-hong
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b. US20030104529A1
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89.5%;
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Pred. No. 1.3e+02;
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US-09-961-527A-6/c
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SEQ ID NO 6
LENGTH: 8091
                                   Matches
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APPLICANT: Turgeon, B. Gillian
APPLICANT: Yoder, Olen
APPLICANT: Yoder, Olen
APPLICANT: Wu, Jianguo
TITLE OF INVENTION: Fungal target genes and methods to identify those genes
FILE REFERENCE: TM0129-0T
CURRENT APPLICATION NUMBER: US/09/961,527A
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/234,673
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
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APPLICANT: Turgeon, B. Gillian
APPLICANT: Yoder, Olen
APPLICANT: Wu, Jianguo
TITLE OF INVENTION: Fungal target genes and methods to identify those genes
FILE REFERENCE: TM0129-UT
CURRENT APPLICATION NUMBER: US/09/961,527A
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/234,673
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/234,650
PRIOR FILING DATE: 2000-09-22
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les 16; Conservative
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 4 GGGATTCGGAGATTGCG 20
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16; Conservative
                                                 Similarity
                                   Conservative
                                                 73.3%;
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Pred. No. 2e+0
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Pred. No. 2.4e+02;
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Pred. No. 2
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2e+02;
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Maximum DB seq length: 200000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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     /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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Listing first 45 summaries
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             0 US-09-961-527A-6
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0 US-09-770-444-192
0 US-09-770-444-192
0 US-09-778-626-595
US-09-73B-626-595
0 US-09-73B-626-595
0 US-09-73B-626-593
0 US-10-12B-714-563
0 US-10-270-333-67
0 US-09-73B-626-1
10 US-09-87B-574-1714
0 US-09-87B-574-1714
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US-09-873-880-29
US-10-037-270-446
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Sequence 7, Appli
Sequence 29, Appl
Sequence 6, Appli
Sequence 1, Appli
Sequence 1732, App
Sequence 175, App
Sequence 192, App
Sequence 192, App
Sequence 595, App
Sequence 563, App
Sequence 563, Appli
Sequence 3, Appli
Sequence 1714, Appli
Sequence 1714, App
Sequence 35322, A
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Sequence 7, Appli	Sequence 7, Appli	Sequence 6265, Ap	Sequence 7388, Ap	Sequence 7265, Ap	Sequence 7247, Ap	Sequence 14337, A	4	643,	(.)	4		Sequence 330, App	Sequence 273, App			መ	Sequence 2053, Ap	σ	Sequence 604, App	Sequence 807, App	5	e 490	`	Sequence 1, Appli	Sequence 3, Appli

## ALIGNMENTS

RESULT 1 US-09-873-880-7/c

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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (382)
; OTHER INFORMATION: n=A, C
; NAME/KEY: unsure
; LOCATION: (454)
; OTHER INFORMATION: n=A, C
US-09-873-880-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent
APPLICANT: Falco, S. Carl
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: GLYCINE MET
FILE REFERENCE: BB1192 US CIP
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                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Office 97 SEQ ID NO 7
                                                                                Query Match
Best Local :
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                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/873,880 CURRENT FILING DATE: 2001-06-04 PRIOR APPLICATION NUMBER: 09/363,321 PRIOR FILING DATE: July 28, 1999 PRIOR APPLICATION NUMBER: 60/094,839 PRIOR APPLICATION NUMBER: 60/094,839 PRIOR FILING DATE: July 31, 1998
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                           LENGTH: 495
TYPE: DNA
ORGANISM: Glycine max
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2 AGGGATTCGGAGATTGCG 20
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53 AGGGGATTTGGAGGTTGCG 33
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17; Conserv
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89.5%;
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Pred. No. 1
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                                                                 Mismatches
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RESULT 2 US-09-873-880-29/c

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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDER: 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00408
FILING DATE:
PRIOR APPLICATION NUMBER: 08/181,492
FILING DATE: 13-7340ary-1994
APPLICATION NUMBER: TCS-203-PCT(94,664-A)
FILING DATE: 13-7340ary-1994
APPLICATION NUMBER: 30,237
RESISTRATION NUMBER: 30,237
RESERBENCE/MOCKET NUMBER: TCS-203-PCT(94,664-A)
FILECOMMUNICATION INFORMATION:
REPERBENCE/MOCKET NUMBER: 30,237
RESERBENCE/MOCKET NUMBER: TCS-203-PCT(94,664-A)
FILECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAN: 617-345-9110
INFORMATION FOR SED ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 base pairs
TYPP: nucleic acid
STRANDEDESS: single
TYPP: nucleic acid
STRANDEDESS: single
TYPP: nucleic acid
STRANDEDESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE:
FAITHE:
NAME/KEY:
LOCATION:
NAME/KEY:
LOCATION:
NAME/KEY:
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US-08-181-492B-25/c
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US-09-221-017B-862
RESULT 14
US-08-181-492B-26
; Sequence 26, Application US/08181492B
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Best Local S
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                                                                                                                                              Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 276 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: IBM CC Compatible
OPERATING SYSTEM: MS-DOS 6.2
SOFTWARE: WordPerfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Makrides, Savvas C
APPLICANT: Kung, Patrick C
TITLE OF INVENTION: T Cell Antigen Receptor V Region
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TC.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9110
TELEPAX: 617-345-9111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: T Cell Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                         FEATURE:
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/181,492B FILING DATE: 13-January-1994
                                                                                                                                                             Local
                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Yankwich, Leon R. REGISTRATION NUMBER: 30,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                             Similarity
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84.2%;
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Pred. No. 1.5e+02;
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                                                                                                                                                             Score 14.2;
Pred. No. 1.
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RESULT 15
PCT-US95-00408-25/c
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US-08-181-492B-26
                                                                                                                                       Sequence 25, Application.

Sequence 25, Application.

Sequence 27, Application.

GENERAL INFORMATION:

APPLICANT: T Cell Sciences, Inc

APPLICANT: T Cell Antigen Receptor V Region Proteins

FITLE OF INVENTION: and Methods of Preparation Thereof

TITLE OF INVENTION: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5552300
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Makrides, Savvas C
APPLICANT: Kung, Patrick C
TITLE OF INVENTION: T Cell Antigen Receptor V Region
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Yankwich, Leon R.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TC: TELECOMMUNICATION INFORMATION: 617-345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
             COUNTRY: United States of America
ZIP: 02194-2775
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: T Cell Sciences
STREET: 1515 Fourth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/181,492B FILING DATE: 13-January-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                      STATE:
                                                                                                         CITY: Needham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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IBM PC Compatible
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84.2%;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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; TYPE: DNA; ORGANISM: Papilloma US-09-000-266-3
FILE REFERENCE: 8484-0037-999

CURRENT APPLICATION NUMBER: US/09/628,099

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 09/000,266

PRIOR FILING DATE: 1998-10-19

PRIOR APPLICATION NUMBER: DE 195 26 386.3

PRIOR FILING DATE: 1995-07-19

NUMBER OF SEQ ID NOS: 30
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US-09-628-099-3/c
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: Shamanin, Vladimir
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              Sequence 3, Applic Patent No. 6368832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.(
Matches 17; Conservative
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LENGTH: 419
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                                                                                                                                                                APPLICANT: Shamanin, Vladimir
APPLICANT: Deviliers-Zur Hausen, Ethel-Michele
APPLICANT: Dev Hausen, Haraid
TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 6484-0037-999
CURRENT APPLICATION NUMBER: US/09/628,099
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/000,266
PRIOR FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: DE P 195 26 386.3
PRIOR FILING DATE: 1995-07-19
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Papilloma virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES THE REFERENCE: 8484-0037-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (1)...(417)
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Zur Hausen, Harald
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Pred. No. 1.2e
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Pred. No. 1.2e+02;
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RESULT 12
US-09-221-017B-862/c
US-09-221-017B-862/Application US/09221017B
; Patent No. 6444799
; Patent No. 6444799
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LENGTH: 419
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Best Local
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FILING DATE: 31-DEC-1997

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PP1546

FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION WHER: PP2911

FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: PCT/AU98/01023

APPLICATION NUMBER: PCT/AU98/01023

APPLICATION DATE: 10-DEC-1998
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                                                                                  LENGTH: 3363 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic
HYPOTHETICAL: NO
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
                                                     ORIGINAL SOURCE
                                                                   ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                    ORGANISM:
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17; Conserv
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                                                                                                       DNA (genomic)
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Pred. No. 1
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LENGTH: 4403765
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Best Local !
                                                                                                                                                         sequence 1, Application US/09103840A Patent No. 6294328
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
                                                                                                                                                  GENERAL INFORMATION:
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Best Local :
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILLING DATE: 1998-06-24
                                                                                                                APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
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SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
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LOCATION: (101753)...(101996)
NAME/KEY: CDS
LOCATION: (110324)...(110439)
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les 17; Conserv
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CDS
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CDS
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85.0%;
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Pred. No. 1
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Pred. No. 64;
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                   RESULT 9
US-09-000-266-3/c
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; LOCATION: (1)...(417)
US-09-000-266-1
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Best Local S
Matches 17
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CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
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                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Zur Hausen, Harald
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
FILLE REFERENCE: 8484-0037-999
CURRENT EPPLICATION NUMBER: US/09/000, 266A
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/DE96/01369
EARLIER APPLICATION NUMBER: DE P 195 26 386.3
EARLIER FILING DATE: 1995-07-19
EARLIER FILING DATE: 1995-07-19
VINDER OF SERVING DATE: 1995-07-19
                                                      TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY FILE REFERENCE: 8484-0037-999
CURRENT APPLICATION NUMBER: US/09/000,266A
CURRENT FILING DATE: 1998-10-19
                                                                                                                                                            APPLICANT: Shamanin, Vladimir
APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
APPLICANT: Zur Hausen, Harald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shamanin, Vladimir
                 EARLIER APPLICATION NUMBER: PCT/DE96/01369
EARLIER FILING DATE: 1996-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Papilloma virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 419
TYPE: DNA
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17; Conserv
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81.0%;
DE P 195 26 386.3
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Pred. No. 1
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Pred. No. 64;
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                                                                                                                       ВY
                                                                                                                       SUCH VIRUSES
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RESULT 3
US-09-134-246-6/c
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                                                                                                                                                                                                                        ; MOLECULE TYPE: cDNA PCT-US96-10521-14
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PCT-US96-10521-14
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Best Local S
Sequence 6, Application US/09134246B
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Best Local
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APPLICATION NUMBER: II 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: II 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: II 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: II 117,932
PRIOR APPLICATION NUMBER: II 117,932
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TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 14
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: IL 1:
FILING DATE: 16-APR-1996
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 1:
FILING DATE: 16-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2887 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MO
TITLE OF INVENTION: AN
UMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.5%; nes 19; Conservation
                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 TAGGGGACTCGGAGACTGCGA 241
                                                                                                    1 TAGGGGATTCGGAGATTGCGA 21
                                                                                                                                                     l Similarity
19; Conserv
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EDNESS: single
                                                                                    TAGGGGACTCGGAGACTGCGA 241
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                          linear
                                                                                                                                                                     84.8%;
90.5%;
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Pred. No. 3
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Pred. No. 3
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GENERAL INFORMATION:
APPLICANT: Wayne, Jay
APPLICANT: X1, Shuang-yong
TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
TITLE OF INVENTION: Wethod For Construction of Two Thermus Plasmid
TITLE OF INVENTION: Replication origins
FILE REPERENCE: Thermus Shuttle Vector
CURRENT APPLICATION NUMBER: US/09/134,246B
CURRENT FILING DATE: 1998-08-14
NUMBER OF SED ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: DNA
ORGANISM: Thermus sp.
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; Sequence 1, Application US/09426290 
; Patent No. 6410712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 42571
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: et al.
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001169
CURRENT APPLICATION NUMBER: US/09/810,347
CURRENT FILING DATE: 2001-03-19
                                                                       GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
                                    SOFTWARE: FastSEQ
SEQ ID NO 1
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SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 168575
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 17; Conserv
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85.0%;
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Pred. No. 1e+0
0; Mismatches
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Pred. No. 81;
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ORGANISM: Homo Sapiens

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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s derived by a
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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21
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Match Length DB
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                    than or equal to the score of the result bein by analysis of the total score distribution.
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1278.561 Million cell updates/sec
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US-09-134-246-6
US-09-810-347-6
US-09-826-290-1
4 US-09-103-840A-2
4 US-09-103-840A-1
            US-09-000-266-1
US-09-08-099-3
US-09-628-099-3
US-09-628-099-3
US-09-628-099-3
US-09-628-099-3
US-08-181-4928-26
PCT-US-95-004-08-25
US-09-193-792-2
US-09-193-792-1
US-09-183-792-1
US-09-34-181-1
US-09-34-24-38-8
US-09-419-568F-8
US-09-419-568F-8
US-09-344-24-38-8
US-09-344-24-38-8
US-09-144-085-3
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            Sequence 14, Appli
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US-08-983-502-14
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CITY: V
            NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WAI
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US-08-639-857-32	US-08-469-260A-11	US-08-920-828-22	US-08-362-577C-22	US-08-921-177-22	US-08-920-827-22	US-08-920-812-22	- 1	US-09-553-132-1	US-08-935-433-1	US-08-185-828A-11	US-08-185-828A-22	US-08-487-727A-1	US-08-470-179-162	US-09-598-326-32	US-09-062-451-32	US-08-991-789A-32	US-09-103-840A-1
Sequence 32, Appl	Sequence 11, Appl	Sequence 22, Appl	Sequence 22, Appl	Seguence 22, Appl	-	Sequence 22, Appl		Sequence 1, Appli	Sequence 1, Appli	Sequence 11, Appl	Sequence 22, Appl	Sequence 1, Appli	Sequence 162, App		`	`	Sequence 1, Appli

ALIGNMENTS

## OPERATING SYSTEM: POLDOS/MS-DOS OPERATING SYSTEM: POLDOS/MS-DOS SOSTWARE: PATENTION DATA: APPLICATION DATA: APPLICATION UNABER: US/08/983,502 FILING DATE: 16-JAN-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US96/10521 FILING DATE: 14-JUN-1996 PRIOR APPLICATION DATA: APPLICATION NUMBER: IL 114,615 FILING DATE: 16-JUL-1995 PRIOR APPLICATION NUMBER: IL 114,986 FILING DATE: 17-AUG-1995 PRIOR APPLICATION NUMBER: IL 114,986 FILING DATE: 17-AUG-1995 PRIOR APPLICATION NUMBER: IL 115,319 FILING DATE: 14-SEP-1995 PRIOR APPLICATION NUMBER: IL 115,319 FILING DATE: 27-DEC-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: IL 116,588 FILING DATE: 27-DEC-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: IL 117,932 PRIOR APPLICATION NUMBER: IL 117,932 GENERAL INFORMATION: APPLICANT: David WALLACH APPLICANT: Mark P. BOLDIN APPLICANT: Tanya M. GONCHAROV APPLICANT: YUTY V. GOLTSEV TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF TITLE OF INVENTION: AND OTHER PROTEINS STATE: D.C. COUNTRY: USA ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER: IBM PC COMP CORRESPONDENCE ADDRESS: Application US/08983502 419 Seventh E: Floppy disk IBM PC compatible Browdy and Neimark 9 Seventh Street N.W., Ste. #1.30 FAS

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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BQ135457.1 GI:20271581

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                                                                             l Similarity
17; Conserv
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Dixon RA
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Insert Length: 936 Std Error: 0.00
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Fax: 580 221 7380
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                                     GGGATTCGGAGATTGCGA 21
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                                                                                                                                                                   /organism="Medicago truncatula"
//db_xref="taxon:3880"
//clone="NF(06E0IEC"
//clone="NF(06E0IEC"
//clone="NF(06E0IEC"
//clone_ib="Elicated cell culture"
//dev_stage="Cell suspensions were subcultured every 14
//dev_stage="Cell suspensions were subcultured every 14
//days. Cells were induced six days after subculture"
//note="vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
72 a 230 c 160 g 274 t
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/strain="var. California"
/db_xref="taxon:54126"
/clone_lib="pristionchus pacificus BAC ends"
a 197 c 146 g 157 t
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1. .936
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Pred. No. 2.2e+03;
                                                                                            Score 16.4; DB 14
Pred. No. 2.3e+03;
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Search completed: July Job time: 163.34 secs
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Matches 18; Conserv
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Arabidopsis thaliana.
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; eudicotyledons; core eudicots;
spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 280)
Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P.,
Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSOOVMG 280 bp DNA linear GSS 28-JUN-1999
Arabidopsis thaliana genome survey sequence T7 end of BAC T10B23 of
TAMU library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                 1 TAGGGGATTCGGAGATTGCGA 21
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AL092470
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                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis
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/db_xref="taxon:3702"
/clone="T10B23"
                                                                                                                                                                                                                                                      /clone_lib="TAMU"
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39 c 43 c
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85.7%;
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Stanford University
855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
Fax: 650 725 8221
                             598
LD09736.5prime LD Drosophila
Drosophila melanogaster cDNA
                                                                                                                                                                                   w
              Drosophila melanogaster
AA390970
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Walbot V
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                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                            /note="Organ: leaf; vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI Site_2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                              ampicillin."
162 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tlssue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
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94.4%;
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melanogaster embryo BlueScript
clone LD09736 5prime, mRNA seg
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sequence from source sequenc
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a; Poales; Poaceae;
                                                                                                                                                                                                                                               Length 441;
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JOURNAL
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SOURCE
ORGANISM
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Best Local
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17; Conserv
                                                               Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TAGGGGATTCGGAGATTG 18
                                                                                                                                                                                                                                                     Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R., Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A., Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J. A BAC-based genetic linkage map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                  Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 598)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,F
                        Class: BAC ends
                                                                                                                                                                                                            Unpublished (2002)
                                                                                                                                                                                                                                  pacificus
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pristionchus pacificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic, DNA
BH823627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACPP2-G06.y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.fruitfly.org/EST, plate: 97 row: C column: 12 High quality sequence stop: 469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawrence Berkeley
One Cyclotron Rd,
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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                                           Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                      Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       вн823627.1 GI:21001370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                               (bases 1 to 722)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: embryo; Vector: BlueScript SK; Site_1: EcoRI Stie_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in BlueScript SK(+/-)"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDcln009023"
/db_xref="taxon:7227"
/clone="LD09736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
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94.4%;
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Berkeley, CA 94720, USA
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era; Muscomorpha;
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1 (bases 1 to 297)

2 1 (bases 1 to 297)

2 2 1 (bases 1 to 297)

RS Konno, H. Aizawa, K. Akahira, S., Akiyama, J., Arakawa, T., Carninci F., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, J., Itah, M., Itah, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Sakai, C., Sato, K., Shibata, Y., Sugnoda, Y., Watahiki, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Sunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, RIKEN Mouse ESTS (Konno, H., et al.)
Unpublished (2000)

RIKEN Mouse ESTS (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 TAGGGGTTTCGGAGATTG 16
                                                                                                                                                                                                                                                                                                                                                               Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Nishlyama.y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibatta,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibatta,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB214821 RIKEN full-length enriched, adult male a musculus cDNA clone A530023C12 3', mRNA sequence.
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                                                                                                                                                                                                                           High-efficiency full-length cDNA cloning. Methods Enzymol. 19-44 (1999)
                                                                                                                                                                                                                                                                                   Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y.
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                                                                                                                                                                                              Please visit our web site (http://genome.rtc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, adult male aorta
                                /db_xref="taxon:10090"
/clone="A530023C12"
                                                                                    /organism="Mus musculus"
                                                                                                                                         Location/Qualifiers
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94.48;
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Pred. No. 1
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1.7e+03;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                Srinivasan, J., Sinž, W., Lanz, C., Brand, A., Nandakumar, R., Raddatz, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A., Jesse, T., G., Willare, J., de Both, M., Schuster, S.C. and Sommer, R.J. A BAC-based genetic linkage map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601391
Fax: 00497071601498
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   Conservative
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                                                                                                      /strain="var. California"
/db_xref="taxon:54126"
/clone 115-"-
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129 c 66 g 83 t
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/dev_stage="adult"
/lab_host="DH10B"
               78.18;
94.48;
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94.4%;
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0; Mismatches 1
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Pred. No. 1.8e+03;
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Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 1261)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                         L Similarity
18; Conser
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   BB171058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 212.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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                                                                                                                                                                                                                                      /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GcCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 342 c 382 g 217 t 2 others
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a 341 c 253 g 212 t
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/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:4585781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, R. Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, R. Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, R. Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, R. Yasunishi, A., Yokota, T., Yasunishi, A., Yokota, T., Yasunishi, A., Yokota, M., Yokota, M., Yokota, K., Yasunishi, A., Yasunishi, Y., Yokota, M., Yokota, K., Yasunishi, A., Yasunishi, Y., Yokota, K., Yasunishi, A., Yasunishi, A., Yokota, M., Yokota, K., Yasunishi, Y., Yasunishi, Y., Yasunishi, Y., Yokota, M., Yasunishi, Y., Yasunishi, Y., Yokota, M., Yasunishi, Y., Yasunishi, Y., Yokota, Y., Yasunishi, Y., Yasunis
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Apad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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Carrinci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Contact: Robert Strausberg, Ph.D.
                                                                                                                            Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 939)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM13314 row: c column: 20
High quality sequence stop: 512.
Location/Qualifiers
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Tissue Procurement: ATCC/DCTD/DTP
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   Procurement: Mark Maconochie,
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                                                                                                                                                                                                                                                                     source
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM13799 row: j column: 18
                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2410 row: n column: 05 High quality sequence stop: 564. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 999)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5', mRNA sequence.
BQ672783
BQ672783.1 GI:21783617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ672783 999 bp mRNA linear EST 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ./organism="Mus musculus"
//db_xref="taxon:10090"
//clone_lib="NMAGE:6336113"
//clone_lib="NHLMGC_130"
//lab_host="DH10B (phage-resistant)"
//lab_host="D10B (phage-resistant)"
//note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/site_1: EcoRV; Site_2: Not1; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is a
NIH_MGC Library."
50 a 197 c 281 g 210 t 1 others
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="hH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:6257092"
/clone_lib="NIH_MGC_102"
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No. 1.5e+03;
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Matches
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                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                           No s1 sequence available.

This clone (DKFZp513F1234) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s. wiemann@dkfz- heidelberg.de; sequenced by EMGL (European Molecular Biology Laboratories, Heidelberg/German) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 522)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S. EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.) Unpublished (1999)
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DKFZp313F1234_r1 313 (synonym: hlcc2) Homo
DKFZp313F1234 5', mRNA sequence.
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                      Similarity
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TAGGGGATTCGGAGATTGCGA 21
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nilarity 90.5%;
Conservative
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                                                                                                                                                                   /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection" 116 c 133 g 149 t 4 others
                                                                                                                                                                                                                                /clone="DKF2p313F1234"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pTriplex2; Site_1: SfiIA;
cDNA-collection"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="686 (synonym: hlcc3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="DKF2p686E18155"
                                                                               84.8%;
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                                                             Score 17.8; In Pred. No. 4.6e 0; Mismatches
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Pred. No. 4.4e
0; Mismatches
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                                                                                   4.6e+02;
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                                                                                                      Length 522;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ821487 697 bp DNA linear GSS 20-FEB-200 2M0094H14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0094H14 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0094 row: H column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 697)
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Fax: 801 585 7177
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                                                                                 Similarity
                  TAGGGGATTCGGAGATTGC 19
                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 697
Location/Qualifiers
                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                              chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." a 189 c 157 g 167 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/60"
/db_xref="faxon:10090"
/clone="UUGC2M0094H14"
/clone_lib="Mouse 10%b plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex≖"Male"
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94.7%;
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                                                           Score 17.4; DB 17; Pred. No. 7.5e+02; 0; Mismatches 1;
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## ALIGNMENTS

RESULT 1
AL702116
LOCUS
DEFINITION ACCESSION VERSION KEYWORDS SOURCE COMMENT REFERENCE TITLE AUTHORS ORGANISM JOURNAL Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s. wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available. Wiemann, S.)
Unpublished (1999) AL702116 421 bp mRNA DKFZp686E18155\_r1 686 (synonym: hlcc3) DKFZp686E18155 5', mRNA sequence. Mammalia; Eutheria; 1 (bases 1 to 421) Homo sapiens Eukaryota; M Contact: Bloecker H EST (Bloecker, H., Bloecker, H., human. AL702116.1 GI:19685471 Metazoa; Boecher, M., Brandt, P., Mewes, W., Boecher, M., Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. Brandt, P., A linear EST 22-MAR-2002 Homo sapiens cDNA clone Mewes, H.W., Weil, B. and Wiemann Weil, B. and

Ler Inc	Length E	Length 811; Indels 0; Gaps 0;	Search completed: July 8, 2003, 03:11:11 Job time : 21.9513 secs	Qy 2 AGGGATTCGGAGATTGCGA 21	Query Match 80.0%; Score 16.8; DB 24; Length 811; Best Local Similarity 90.0%; Pred. No. 1e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpC-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory contemps etc., particularly by detecting mutations or single nucleotide CC polymorphisms (SNP's), and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

CC method for determining the degree of cytosine methylation described in
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                                                                                                                                                                                                                                                                                                                                         Claim
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                    This invention describes a novel method for determining the degree of commethylation of a particular cytosine in a motif 5'-Cp0-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one cand the degree of hybridisation to both classes is determined from the call and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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gastrointestinal; respiratory system; single nucle
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05-SEP-2000;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'CQG-3', present in a genomic sample of DNA. The sample is treated themically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The metho is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorder of the central nervous, cardiovascular, gastrointestinal and respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
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05-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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2000DE-1044543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for detecting cytosine methylation
                                                                                                                                                                                                                                                           Sequence Listing; 56pp;
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of
                                                             The method
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This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpC-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil. then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory cystems etc., particularly by detecting mutations or single nucleotide CC polymorphisms (SNP's); and (ii) for differentiation. The method allows the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
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05-SEP-2000;
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                     WPI; 2001-483426/52.
                                                      (HUMA-) HUMAN GENOME SCI INC
                                      Barash SC,
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2000US-0246477.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and

cytosine methylation

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RESULT 11
ABL32794
ID ABL32794
ID ABL33794
AC ABL33
AC AB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45017 BP; 12919 A; 10037 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 767.
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                                                      Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                  WPI; 2002-130909/17
                                                                                                                                                                                                               Olek
                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
01-SEP-2000;
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2000DE-1043826
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Pred. No. 40
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bowel disease;
                                                         gene, useful
abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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AAK77217 standard; DNA; 45017 BP
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   17-JAN-2001; 2001WO-US01354
                                      09-AUG-2001.
                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer.
cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent sequences used in the exemplification of the present invention.
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                                                                    WO200157182-A2
                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 32029.
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19; Conserv
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     05-SEP-2000

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04-FEB-2000;
24-FEB-2000;
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26-JUL-2000;
14-AUG-2000;
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2000US-0232081
2000US-0232981
2000US-0233397
2000US-0233398
2000US-0233400
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2000US-0217487.
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2000US-0227182.
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2000US-0225447.
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2000US-0234998.
2000US-0235484.
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2000US-0225213
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     2000US-0236370
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RESULT 9
AAK77216; standard; D
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AAK77216;
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AC AAK77216;
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DT 07-NOV-2000 (first
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cytostatic; gene therapy; vaccine; metastasis; ds.
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     2000US-0190176

2000US-0198123

2000US-0205515

2000US-0214886

2000US-02114886

2000US-02114880

2000US-02114880

2000US-0217496

2000US-0217496

2000US-0224518

2000US-0224518

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2000US-0225757

2000US-0225718

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2000US-0236369
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RESULT 8
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Best Local S
Matches 19
                viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosi cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disability respiratory distress syndrome; inflammatory bowel disability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200129232-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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14-AUG-2000; 2000US-0225564
                                                                                                                                                                                                                                           Human cDNA differentially expressed in granulocytic cells #1294
                                                                                                                                                                                                                                                                                                                 14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK84723 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cordell B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCIO-) SCIOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-2000; 2000WO-US28941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-290920/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
                                                                                                                                                                                      SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE00605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGGGGATTCGGAGATTGCGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGGGGACTCGGAGACTGCGA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2887
                                                                                                                                                                                   granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 15; 116pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99us-0160559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA; 2887
                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.8%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.8;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ი</u>
                          inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2887;
                                                                                      thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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TAGGGGACTCGGAGACTGCGA 241 TAGGGGATTCGGAGATTGCGA 21 Conservative

Mismatches

2;

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CG GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent CG that alters the expression of at least one gene in Gs; (2) screening (M3) CC for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammation (especially CC chronic) or in a tissue, an allergic response in a subject period or sterile inflammation (especially chronic) or in a tissue, or sterile inflammation of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, or sterile inflammatory disease, by contacting a tissue having considered to a pathogen or sterile inflammation in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject capable of modulating GCA preferably in an inflammation in a tissue, an allergic response in a subject, exposure of a subject of a pathogen or sterile conflammatory disease, corporate in a tissue, an allergic response in a subject, exposure of a subject of a pathogen or sterile conflammatory disease, corporate in a corporate in a subject of modulating GCA preferably in an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject of a pathogen or sterile conflammatory bowel disease, crohn's disease, relative ocitits, promotome, in the sequence represents a gene differentially expressed in granulocytes. Of the printed conflammatory death of the above condition in para
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 19
                                                                                                                              of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/spublished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GCA), by detecting the level of expression of gene(s) (Gs) id DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beazer-Barclay Y, Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             granulocyte activation; chronic inflammation; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxicity
  l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID No 1294; 114pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-237189P
                                                                                          BP;
                                                                                          853 A; 595 C; 625 G;
                     84.8%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MS
                     Score 17.8;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamaga S,
                                                                                          814 T;
                             ω6;
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                                              24;
                                                                                          0 other;
                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Gs) identified by
                                                2887;
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RESULT 6
AAT61405
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expresses an mRNA and protein product. The promoter Region 1 sequence is located upstream (5') to exon 1, which is the alternatively-spliced 5' untranslated region (UTR) that is less commonly used. The promoter Region 2 sequence is located downstream (3') of exon 1 and upstream of exon 2, which is the more commonly used 5' UTR. The CASPB gene has been localized to human chromosome 2933-34. The methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding functional CASPB in only a vector that is diagnosed or treated is a tumour in which a myc gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inactivation of a caspase-8 (CASP8) gene is determined by detecting a modification of CASP8 genomic DNA that results in inactivation of the gene. CASP8, a cysteine protease, is part of the death inducing signaling complex (DISC) associated with the Fas receptor. CASP8 is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASP8 promoter region sequences, in particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation. Methylation PCR can be used to examine even minute amounts of patient material to demonsrate whether the CASP8 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene
                                                                                                                                                                                                                                                                                      MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death; antibody; FAS ligand receptor; FAS-R; death domain region; septic shock; tumour necrosis factor; tumour; HIV-infection; oligodendrocyte death; tumour sprogrammed cell death; p55-R; graft rejection; acute hepatitis; apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis; autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 97-98; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            MACH isoform alphal coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT61405 standard; cDNA; 2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASP8 gene is also provided
                  14-JUN-1996;
                                                        06-FEB-1997
                                                                                               WO9703998-A1
                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                       therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B₽;
                                                                                                                                                                                                                                                                           SS.
                  96WO-US10521.
                                                                                                                                                                        Location/Qualifiers 291..1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 A; 204 C;
                                                                                                                                  /product= MORT-1 binding
                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.8;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 G; 238 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                  protein (MACH) isoform alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 7
AAD03915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC isoforms of MACH. MACH is a binding protein for the mediator of receptor CC toxicity (MORP-1) protein. MORT-1 binds to the FAS ligand receptor CC (FAS-R) death domain region, and triggers part of the cell death CC signalling cascade in mammalian cells. Vectors containing these CC sequences, the encoded proteins, and antibodies (Ab) against them are CC sequences, the encoded proteins, and antibodies (Ab) against them are CC used to modulate the effect of FAS-R ligand or TNF on cells that carry CC FAS-R or p55-R. This is specifically for treating tumours, HIV infected CC cells or other diseased cells, by control of apoptosis/programmed cell CC death. The encoded proteins are mediators of the cell death pathway CC initiated by TNF and FAS-R binding, i.e. it mimics or enhances the CC effect of MORT-1 where increased cytotoxicity is required. To inhibit the CC care hepatitis, sequences encoding antisense molecules or ribozymes, or CA bagainst the protein, are used. Compounds that inhibit MACH are Optentially useful for controlling MACH activity e.g. in cases of autoimmune disease, oligodendrocyte death in multiple sclerosis or CC ADS-inhibited T-cell suicide. The MACH proteins can also be used to isolate and characterise other proteins and receptors involved in CC signalling and for Ab production. The Ab can be used to purify the new CC proteins and for diagnosis of conditions involving abnormal function of CC CAS-R mediated cellular effects
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1996;
16-JUL-1995;
17-AUG-1995;
14-SEP-1995;
27-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WEIN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-132570/12.
P-PSDB; AAW11891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boldin M,
            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 116-117; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding MACH protein that interacts with MORT-1 protein to mediate intracellular effects of FAS or TNF receptors, partic
                                                        Homo sapiens
                                                                                                   cysteine
                                                                                                                                               Human
                                                                                                                                                                           02-JUL-2001
                                                                                                                                                                                                         AAD03915;
                                                                                                                                                                                                                                     AAD03915 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT61396, and AAT61405-T61411 represent coding sequences
                                                                                    tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for regulating apoptosis in tumours,
                                                                                                                                                                                                                                                                                                               221
                                                                                                                                             caspase-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             mediated cellular effects.
                                                                                                                 caspase-8; MACH; FLICE;
                                                                                                                                                                                                                                                                                                                                          1 TAGGGGATTCGGAGATTGCGA 21
                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEINWURZEL YEDA RES &
                                                                                                                                                                                                                                                                                                                                                                        Similarity 90.
19; Conservative
                                                                                    cathepsin
                                                                                                                                                                                                                                                                                                            protease;
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 853 A; 595 C; 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96IL-0117932.
95IL-0114615.
95IL-0114986.
95IL-0115319.
95IL-0116588.
                                                                                                                                               DNA.
         Location/Qualifiers 292..1731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEV
                                                                                                                                                                                                                                    DNA;
                                                                                                 apoptosis; caspase expression cassette; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                      84.8%;
90.5%;
                                                                                 urokinase; proliferation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CO
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                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                 Mch3;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   2 17.8; L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wallach
                                                                                                                                                                                                                                                                                                                                                                                                                                  814
                                                                                                                                                                                                                                                                                                                                                                                                    DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Τ;
                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells etc.
                                                                                                                                                                                                                                                                                                                                                                                                    2887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 partic.
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                                                                                                                                                                                                                                                                                                                                                                      Gaps
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CC analyzed using methylation sensitive PCR analysis. Amplification of the CC 5' untranslated region (UTR) of the Casp8 gene was performed in reaction CC mixtures containing bisulfite treated DNA. Primers AAA51818-23 were CC designed to produce a 320 bp fragment in the upstream region of Casp8 CC gene extending from nucleotides +221 to +541. Wild type primers were CC used to amplify the corresponding region of untreated genomic DNA. CC Controls without DNA were also performed. CASP8, a cysteine protease, is CC part of the death inducing signaling complex (DISC) associated with the CC particular Region 1 and Region 2, are crucial to the design and execution CC of the genomic methylation PCR analysis of CASP8 gene inactivation. CC Methylation PCR can be used to examine even minute amounts of partient material to demonstrate whether the CASP8 gene expresses an mRNA and CC protein product. The CASP8 gene has been localized to human chromosome CC 433-34. The methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding CC functional CASP8 in cells. The cancer that is diagnosed or treated is a tumour in which a myc gene is amplified, such as a neuroblastoma. CC Aggressive neurobastoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated
RESULT 4
ABNS8902
ID ABNS
XX
AN ABNS
XX
AN ABNS
XX
DT 15-0
DT 15-0
DT 15-0
CX
DT 01-1
CX
DT 02-1
CX
DT 03-1
CX
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Investigation of silencing of caspase-8 (CASP8) gene by methylation was analyzed using methylation-sensitive PCR analysis. Amplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 61; 107pp; English.
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                                                                                                                                                                                          28-JUL-2000; 2000US-221607P
02-MAY-2001; 2001US-287724P
      WPI; 2002-257383/30
                                                                  Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                       20-JUL-2001; 2001WO-IB01903
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200210449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human spliced transcript detection oligonucleotide SEQ ID NO:31650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN58902 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse; rat; splice transcript; detection;
variant; transcriptome; oligonucleotide l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                 COMPUGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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                                                                     Mintz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 3
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                                                                  Ħ
                                                                     Mintz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                               Faigler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA transcript,
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В QΥ

Sequence

60 BP; 14 A; 8 C; 28 G; 10 T; 0 other;

Score 17.8;

DB 24;

Length

60;

0

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messenger RNAs that populate a (sub-)transcriptome, where the cc (sub-)transcriptome comprises messenger RNAs transcribed from multiple ct transcription units that populate a genome. The library comprises cc several oligonucleotides, each capable of hybridising selectively to a cc the genome, which encodes one or more messenger RNAs plice variants. Cc The oligonucleotide libraries are useful for detecting mRNAs from a cc biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in cc detecting RNA transcripts and splice variants of human or animal cc libraries to detect transcripts of a sub-transcriptome under a cc particular biological or pathological state, and so allowing the corresponding transcriptome conjugation of tissue and pathology-specific genes such as those genes conjugation; to detect developmental specific genes such as those genes conjugation; to detect developmental specific pathological transcripts and splice variants of a man to detect RNA transcripts and splice variants of a pattent suffering condition; to detect developmental specific pathological condition; to detect deve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID 31650; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present
                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         describes oligonucleotide libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting
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RESULT 5
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Best Local S
Matches 19
                                                                                                                                                                                                                        CASP8; caspase-8; promoter; Region 2; inactivation; methylation; Cysteine protease; tumour suppressor; chromosome 2q33-34; neurob cancer; death receptor; apoptosis; cytostatic; gene therapy; ss.
                                                                                                                                                                                                                                                                                 CASP8 promoter Region
WPI; 2000-452423/39
                            Kidd VJ,
                                                                                                                                         06-JUL-2000
                                                                                                                                                                    WO200039347-A1
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                              31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                       AAA51793 standard; DNA; 753
                                                                                  31-DEC-1998;
                                                                                                             30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAGGGGATTCGGAGATTGCGA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
19; Conserv
                                                       TS
                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGGGGACTCGGAGACTGCGA 39
                          Lahti JM,
                                                     JUDE CHILDREN'S RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                  98US-0114308
                                                                                                             99WO-US31280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.8%;
                            Teitz T;
                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred
                                                       HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                         neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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AC XXX DT XXX DX

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RESULT 2
AAA51820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising the CASP8 gene that results in inactivation of the gene
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                                                                   WPI; 2000-452423/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sense primer for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21
Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200039347-A1
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                                                                                                                                                                                                       (SJUD-)
                                                                                                                                                                                                                                                                           31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                              30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor; apoptosis; cytostatic; gene therapy; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAGGGGATTCGGAGATTGCGA 21
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                                                                                                                                                                                                       ST JUDE CHILDREN'S RES HOSPITAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                           98US-0114308
                                                                                                                                                                                                                                                                                                                                              99WO-US31280
                                                                                                                                   JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CASP8 unmethylated-specific bisulfite treated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
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Pred. No. 0.86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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WPI; 2000-452423/39

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AAA51822
ID AAA5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canalyzed using methylation sensitive PCR analyzis. Amplification of the Caspa gene was performed in reaction CC for untranslated region (UTR) of the Caspa gene was performed in reaction CC mixtures containing bisulfite treated DNA. Primers AAA51818-23 were CC designed to produce a 320 bp fragment in the upstream region of Caspa CC gene extending from nucleotides +221 to +541. Wild type primers were CC controls without DNA were also performed. CASPB, a cystelne protease, is CC part of the death inducing signaling complex (DISC) associated with the CASPB receptor. CASPB is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASPB promoter region sequences, in CC particular Region i and Region 2, are crucial to the design and execution CC of the genomic methylation PCR analysis of CASPB gene inactivation. CC Methylation PCR can be used to examine even minute amounts of patient CC aga-33.4. The methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding CC functional CASPB in cells. The cancer that is diagnose cancer. Cancer is C lung carcinoma, non-small-cell lung carcinoma, coloractal carcinoma, juvenile neuroblastoma (preferred), small-cell contering cervical carcinoma and be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated CC apoptosis in cells containing an inactivated CASPB gene is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene
                                                                                                                                                                                                                                                                                          CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 61; 107pp; English
                                               Kidd VJ,
                                                                                                                   31-DEC-1998;
                                                                                                                                                      30-DEC-1999;
                                                                                                                                                                                        06-JUL-2000
                                                                                                                                                                                                                         WO200039347-A1
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                               Sense primer for
                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA51822 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Investigation of silencing of caspase-8 (CASP8) gene by
                                                                                (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                 Lahti JM,
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                                                                                                                     98US-0114308
                                                                                                                                                      99WO-US31280
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90.5%;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                   Match Length
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT: *
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT: *
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT: *
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT: *
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AC AAAS
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XX Sens
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KW tumc
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XX WO22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sense primer for CASP8 methylated-specific bisulfite treated
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                                                                                                                               WPI; 2000-452423/39
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BASE COUNT
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KEYWORDS
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-MAR-1994) Hubert Lerivray, Universite de Rennes
URA CNRS 256, Campus de Beaulieu, Rennes 35042, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis.
Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (sites)
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                 788
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                                                                                                                                                                                                                                                                                                                                             /organism="xenopus laevis"
/db_xref="taxon:8355"
/clone="gcdk2"
/clone_lib="genomic library of I.
/dev_stage="adult"
                           /translation="MENFQKVEKIGEGTYGVVYKARNRETGEIVALKKIRLDT" 2442. .>2742 /note="5' region of intron I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:473584
                                                                                                                                                                                                                                                      /note="Using a cat reporter gene the promoter activity in this region was
                                                                        /codon_start=1
/product="protein kinase"
/protein_id="AAA82123.1"
/db_xref="GI:473585"
                                                                                                                                                                              1929. .2325
/gene="cdk2"
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1929, .2441
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Epigenomics AG (DE)
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(NID:g11617019)"
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(NID:g10991125)"
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/note="chemically treated genomic DNA (Homo sapiens)"
548 c 2538 g 3900 t
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(NID:910996436)"
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This submission represents a partial sequence of clone RP23-349P1. Only the unique (non-overlapping) sequence is represented. The remaining sequence overlaps clone RP23-469C2 (AC098839). An overlap of 2kb is included in this submission for reference. Base 10433 to base 19478.
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AC091785
AC091785.5
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On Mar 7, 2002 this sequence version replaced gi:16603978.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-JUN-2001) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA 3 (bases 1 to 178271)
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Bell,M., Baker,J., Santos,L., Miller,B., Katzenberger,F.,
Bell,M., King,L., Yang,C., Dike,S., Palmer,L., O'Shaughnessy,A.
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MCCombie,W.R., Spiegel,L., de la Bastide,M., Preston,R.,
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                                                                                                                                                                                            note="We believe the assembly to be correct. The sequence is covered by a single high quality subclone sequenced with dye terminator chemistry. There is partial coverage by an additional subclone with quality below phred30."
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                                      /note="We believe the assembly to be correct. The sequence is covered solely by a PCR product which was generated with a high fidelity polymerase. The sequence is of high quality."
                                                                                                          sequenced with 136300. .136391
                                                                                                                                                                               complement(125470.
                   136305.
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/clone_lib="RPCI-23"
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/db_xref="taxon:10090"
                                is of high quality.
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sequence from base position 134614 to product of RP11-575C6 BAC DNA.

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                                                                                                                                                                                                   The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscedawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jun 7, 2001 this sequence version replaced gi:13677176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-JUL-2001) Genome University School of Medicine, MO 63108, USA
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Direct Submission
Submitted (07-JUN-2001) Genome
University School of Medicine,
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University School of Medicine,
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Direct Submission
Submitted (19-APR-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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The clone sequenced to the left is RP11-156B7; the clone sequenced to the right is RP11-536I18, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-575C6; actual end is at base position 180956 of RP11-575C6.
                                                                                                                  (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
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Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0575C06
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192. .228
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/db_xref="taxon:9606"
/chromosome="2"
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to08f03.x1"
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4963. .5682
                                                                /note="similar to
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/note="similar
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RESULT 10
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Sequencing vector: M13; 48% Sequencing vector: plasmid; 44% Sequencing vector: plasmid; 44% Chemistry: Dye-primer ET; 48% of reads Chemistry: Dye-terminator Big Dye; 44% of reads Assembly program: Phrap; version 0.990319
                                                                                                                                       Submitted (10-JUL-2000) Genome University School of Medicine, MO 63108, USA On Aug 9, 2001 this sequence ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 179216) Waterston, R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center code: WUGSC
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/gene="SMa0179"
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KKDVWWTVGLAAAALLLFGIOVLINWRLDWLDVPLRLRWMYVKGGLLIFIMLTVANV
IEVFLLGRIFANTYLLAAPVRVGBALRIGDAHGDVLOVSLLDTTLMEFGGEVLWTDH
ALQMEISSTAMIYILAARAPVRVGBARRIGDAHGDVLOVSLLDTTLMEFGGEVLWTDH
PSGRIIKFPNSTVFDTPVFNYSWPLFPYVWNEIKFQLAYESDLEFVARTMREVVEEQV
GDIMSOKYKIYKHILSNTPUDLEVKHHVVHFRVSENTWLEAIVRYLVPPKEAGRTK
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/transi_table=11
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/protein_id="Ask64751.1"
/db_xref="GI:14523156"
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/codon_start=
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                         Sequencing Center, Washington 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Similarity
19; Conserv
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18150)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens BAC clone
AC007256
AC007256.5 GI:14327821
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 <u>₩</u>
                               3 (bases 1 to 181150)
Waterston,R.H.
Direct Submission
Submitted (07-APR-1999) Genome Sequencing Center, Washington
Submitted (07-APR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                           Unpublished 3 (bases 1
                                                                                                                                          2 (bases 1 to 181150)
Du,F., LaPlant,Y., Doebber,A.
The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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82939. .179216
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/db_xref="taxon:9606"
/chromosome="2"
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37637 c 38145
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Pred. No. 1.8e+02
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RP11-575C6 from 2,
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/protein_id="AAK64744 1"
/db_xref="G1:A4523149"
/tdb_xref="G1:A4523149"
/translation="MOREDEYUIGDPEIATVTPLTDRGFYILGNELGSTSVTIFDAEK
NPVGIIDIEVTLDTKLLSSTIRQSVPGSSVKVTSANGRIVLSGSATDAVAATQAEQIA
SRFAGDEEVINSIKITSSQQVQLNVRFYEINRDVGKELGTQISAAYANGNGSVEFNSS
SRFAGDEEVINSIKITSSQQVQLNVRFYEINRDVGKELGTQISAAYANGNGSVEFNSS
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/gene="SMa0162"
/function="Miscellaneous; Unknown"
/note="glimmer prediction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SMa0164"
1569. .1865
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/gene="SMa0162"
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QARVVRAPSSGHFLELQ"
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EFPIPISEQDGTITVSYKKFGVGLDFTPTVLSDGLIALDIEPEVSAIDNTASYRVGNI
AIPGFSVRRARTSVDLKSGQSFMIAGLLQSENNLITQRVPGLGQLPILGALFSSKAYQ
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/plasmid="pSymA"
                                                                                                                                   /product="hypothetical protein?"
/protein_id="AAK64746.1"
/db_xref="GI-1423151"
/translation="MEMTIGASGRSVLJGRSGGGRRPTELVMAIVATVILSSCOTSEVL
SGAEFDPTSALASSGDVSKSDLDQGKLJFMNGNYGLAEKHFRKAVELRQDNAEALMGL
AACYDRLGRFDLADRAYNQLLKVAGRQPRIVNNMGYSQYLRGEKAKARKLLLEARAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SMa0166"
1887. 2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:14523150" /db_xref="GI:14523150" /translation="MIRRSSRPRGEPGLLFASSILLSGCONHELVRSETIALSAGDAI AANSVMOMVDPWPPRVKQTSLATPADLEQYKPQQPNAEQNGGNGETYPNDTTTQ" 1887. .2417
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/protein_id="AAK64743.1"
/db_xref="GI:14523148"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="glimmer prediction"
/codon_start=1
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/function="Structural elements; Cell exterior; surface
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                                                2501.
                                                                                       PGDETIEANLALLDRS"
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/protein_id="AAK64745.1"
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/gene="SMa0168"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="Miscellaneous;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SMa0166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="glimmer prediction"
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RATAHLFSGHRTSPSGGGTTKTPYGLNVGARLGELAEAGFTADEPELIDWTLALDPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANPESLGDPPVATDLLSAAGETSIDEADVQBPVEYGSDVDAAEDALTSLYLVQDALAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MNATKLLLIPLLAAFAYISLVSLTYLSQRALLYPGASATPAPE RASWGQNASIQTPDGETLHGLYSRGEPGQPSVLFFLGNADRVSNYGFFAQALAARGIG LLALSYRGYPGSSGTPNEHGLLIDGIAAFDMLAARSGNEIVVLGQSLGSGVAVDTAKK RPAVAYILVSAYLSVLSLAQTYYPFFVALLTKDPFRSDLKIAGVRQPBAVYPRPARH HPTIVFGRSSYSDRSRAQADAHLRCRPQRSVGCPHG"
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RFGVMFFADPAAAFANIGRAMRPGARLVWMVWQSRERNEWSRAIRQALAPAIAVSAGA
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hypothetical protein"
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5321. .6241
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Tokai University,

Isehara, Kanagawa

24.0 kbp long"

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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Best Local
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  Genomics
21100893
                                                  Hadano,S., Yanagisawa,Y., Skaug,J., Fichter,K., Nasir,J., Martindale,D., Koop,B.F., Scherer,S.W., Nicholson,D.W., Rouleau,G.A., Ikeda,J.-E. and Hayden,M.R. Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2, and ALS2CR3, in the juvenile amyotrophic lateral sclerosis ALS2CR2, critical region at chromosome 2q33-q34: candidate genes for ALS2CR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (17-JUN-1996) D. Wallach, The Weizmann Institute,
Membrane Research & Biophysics, Rehovot 76100, ISRAEL
4 (bases 1 to 2887)
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Submitted (24-MAY-1996) D. Wallach, The Weizmann Institute,
Membrane Research & Biophysics, Rehovot 76100, ISRAEL
Revised by [3]
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                                                                                                                                                                                                                               Homo sapiens DNA.
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AB038981
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19; Conser
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                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA66953.1"
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53 a 595 c 625 g 814 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="MACH-alpha-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="triggers cell death"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                          6502 bp
gene for caspase-8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.8%;
                    200-213 (2001)
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Pred. No. 1.4e
0; Mismatches
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complete plasmid sequence.
AE007203 AE006469
AE007203.1 GI:14523147
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                2 (bases 1 to 10253)
Barnett,M.J., Fisher,R.F., Jones,T., Komp,C., Abola,A.P.,
Barnoy-Hubler,F., Bowser,L., Capela,D., Galibert,F., Gouzy,J.,
Barloy-Hubler,F., Bowser,L., Hyman,R.W., Kahn,D., Kahn,M.L.,
Gurjal,M., Hong,A., Huizar,L., Hyman,R.W., Kahn,D., Kahn,M.L.,
Kalman,S., Keating,D.H., Palm,C., Peck,M.C., Surzycki,R.,
Wells,D.H., Yeh,K.-C., Davis,R.W., Federspiel,N.A. and Long,S.R.
                                                                                                                                                                    Rhizobiaceae; Sinorhizobium.

1 (bases 1 to 1023)
Barnett,M.J., Fisher,R.F., Jones,T., Komp,C., Abola,A.P.,
Barloy-Hubler,F., Bowser,L., Capela,D., Galibert,F., Gouzy,J.,
Gurjal,M., Hong,A., Hulzar,L., Hyman,R.W., Kahn,D., Kahn,M.L.,
Kalman,S., Keating,D.H., Palm,C., Peck,M.C., Surzycki,R.,
Wells,D.H., Yeh,K.C., Davis,R.W., Federspiel,N.A. and Long,S.F.
Wuclectide sequence and predicted functions of the entire
Sinorhizobium mellloti pSyma megaplasmid
Sinorhizobium mellloti pSyma megaplasmid
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Sinorhizobium meliloti
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Hadano, S., Ikeda, J. and Hayden, M.R.
Direct Submission
                                                                                                                                                          21396509
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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/note="CDS is reported
alternative 5'UTR"
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1744. .39:
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/note="intron is approximately
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/db_xref="taxon:9606"
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90.5%;
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and Long, S.R

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 Query Match 84.3
Best Local Similarity 90.3
Matches 19; Conservative
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1 (bases 1 to 2503)

Breckenridge,D.G., Nguyen,M., Kuppig,S., Reth,M. and Shore,G.C.
The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
complex at the endoplasmic reticulum
proc. Natl. Acad. Sci. U.S.A. 99 (7), 4331-4336 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-SEP-2001) Biochemistry, McGill University, 3655 Promenade Sir William Olser, Montreal, PQ H3G1Y6, Canada Location/Qualifiers
                                                                                                                                  1 (bases 1 to 2887)
Wallach, D., Boldin, M., Goncharov, T. and Golstev, Y.V.
Modulators of the function of FAS receptors and other proteins
Patent: US 6399327-A 14 04-JUN-2002;
                                                                                                                                                                                                                                                                     Sequence 14 from patent AR211527
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Breckenridge, D.G., Nguyen, M., Kuppig, S.,
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RVMLYQISEBYSKRSELRFKFILQEBISKÇKLDDMMILDIFIEMEKRVILGBEKLDI
LKRVCAQINKSLLKIINDYEEFSKERSSSLEGSPDEFSNGEELCGVMTISDSPREQDS
ESQTLLKVYQMKSKPRGYCLIINNHNEAKAREKVPKLHSIRDKRGTHLDAGALTITE
ELHFEIKPHDLOCTYEQLYEILKIYQLMDHSNMCDEFICGILSHGDNGIIYGTDQEAFI
YELTSQFTGLKCPSLAGKPKVFFIQACGDNYQKGIIVETDSEEQPYLEMDLSSPQTR
YIPDEADFILGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCFRGDDILTILTEVNYE
VSNKDDKKNMGXQMPDFTELKKKLVEFSD"

528 c 593 g 656 t
                                                                                                     Location/Qualifiers
1. .2887
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/protein_id="AAL87628.1"
/db_xref="Gi:19401519"
/translation="MEGGRRARVVIESRRNFFLGAFPTPFPAEHVELGRLGDSETAMV
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/codon_start=1
                                                                          organism="unknown"
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Pred. No. 1.4e+02;
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US 6399327.
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No. 1.3e+02;
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2 (bases 1
Wallach, D.
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               to 2887)
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90.5%;
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221 TAGGGGACTCGGAGACTGCGA 241
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Cordell,B. and Li,Y.
Functional cloping of genes encoding proteins/enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteclytic cleavage
Patent: WO 0129232-A 15 26-APR-2001;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2887)

Boldin,M.P., Goncharov,T.M., Goltsev,Y.V. and Wallach,D. Involvement of MACH, a novel MORTI/FADD-interacting protease, Fas/APO-1 - and TNF receptor-induced cell death Catalage (6), 803-815 (1996)
                                                                                                                                                                                                                 x98172.1 GI:1403318
cell death; MACH-alpha-1;
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/db_xref="taxon:9606"
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/db_xref="GI:14271066"
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                                                                                                                                                                                                                                                   1 (bases 1 to 982)
Teitz,T., Wei,T., Valentine,M.B., Vanin,E.F., Grenet,J.,
Valentine,V.A., Behm,F.G., Look,A.T., Lahti,J.M. and Kidd,V.J.
Caspase 8 is deleted or silenced preferentially in childhood
neuroblastomas with amplification of MYCN
Nat. Med. 6 (5), 529-535 (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                      Teitz,T., Wei,T., Valentine,V.A., Bo
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens caspase 8 AF210257
                                                                                                                                        Submitted (01-DEC-1999) Tumor Cell Biology, St. Research Hospital, 332 N. Lauderdale, Memphis,
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FQRLQEKRMLEESNLSFLKELLFRINKLDLLITYLNTKKEEMERELQTPGRAQISAYR
VMLYQISEEVSRSELRSFKFLLQEEISKCKLDDDMNLLDIFIEMEKRVILGEGKLDIL
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/note="5' flanking region of caspase 8 gene"
235 c 241 g 308 t
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1.2e+02;
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Homo sapiens caspase-8L mRNA,
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HimejllD., Tsukamoto, H. and Horiuchi, T.
Direct Submission
Submitted (10-MAY-2001) Medicine and Biosystemic Science, Kyushu
University Graduate School of Medical Science, 3-1-1 Maidashi,
Higashi-Ku, Fukuoka 812-8582, Japan
Location/Qualifiers
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                                          Homo sapiens procaspase-BL (CASP8) mRNA, alternatively spliced. AF422925
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                                                                                          03-APR-2002
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Title:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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*:un_db
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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093932 Rattus n	ZZ9I99 Oryza	CO9/846 Rattus n	CIO/2/5 Rattus n	C009256 Drosoph	C130018 Rattus n	L731550 Homo s	C074388 Homo sap	C104166 Homo sap	.C099208 Rattus n	P003379 Oryza sa	C103683 Homo s	.C014163 Drosophi	.C006749 Caenorha	005734 Caulob	177464 Drosoph	60409 H.sapiens	L683814 Mouse D	023987 Homo sap	C099245 Rattus n	P00430/ Oryza sa	P003843 Oryza sa	C091938 Homo sap	3515 Caenorha	007406 Halocynt	C115475 Rattus	731879 Oryza sa	C097575 Rattus n	X345119 Sequenc	.X344611 Sequen	281276 Sequence	07979 Xenopus lae	AC091785 Gen	Formula 96957EX	0/4010 BONO SA	COZIOLE HOMO CAN	ECSEPT HOMO SAP	981/2 H.sapiens	134419 Sequence	211527 Sequen	422925 Homo sap	380342 H	.0257 Homo sap	£422929 Homo sap	Description		

## ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AF422929	RESULT 1
Breckenridge,D.G., Nguyen,M., Kuppig,S., Reth,M. and Shore,G.C. The procaspase-8 isoform, procaspase-8L, recruited to the BAP31	Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 777)	Homo sapiens Rukarvota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;	Homo sapiens.	•	AF422929.1 GI:19401529	AF422929	alternatively spliced.	Homo sapiens clone 4 procaspase-8 (CASP8) mRNA, partial cds:	AF422929 777 bp mRNA linear PRI 03-APR-2002		

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; SEQ ID NO 210
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-210
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US-10-156-761-1/c
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                                              Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed -
NUMBER OF SEQ ID NOS: 550
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CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30
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                                                                                                                                                                                                                                                                                                                                                                     CATTIGGCCCTGGGGGCCGACGGTTAAGTACTTTATTCTGTCATTCTGTCGAATCACGAA 534
                                                                                                                                                                                                                                                                                                                                                                                                         MBSSDAHNSTSS.STHW....G.YCH....TMYSBS..AYN.C..YH.D.T.B.SKH...
IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Godowski, Paul J.
Gurney, Austin L.
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l23; Mismatches
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LENGTH: 9025608
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces avermitilis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                  8877178 CTCCTGTCTGCCCTGTCTGTCGTCGGTCCCGCCTGCCCTTCCCTGCCTTTCCCG
8877058 A 8877058
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                                     395 A 395
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                                                                                                                                                                                                                                                              Length 9025608;
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Search completed: July 8, 2003, 06:03:34
Job time: 448.299 secs

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 547
; LENGTH: 6146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-428-547
                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-800-631-96
J Sequence 96, Application US/09800631
J Sequence 96, Paper No. US20020082228A1
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                                                                                                                 CURENT APPLICATION NUMBER: US/09/800,631
CURENT ELIUNG DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US/09/657,346
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 175
SEQ ID NO 96
LENGTH: 30310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.6%;
Best Local Similarity 45.0%;
Matches 131; Conservative
                                                                                                                                                                                                                                                    APPLICANT: Hong Zhang
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ATTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1019
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                NAME/KEY:
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                                                                                     ORGANISM: Mus musculus
                                                                                                        TYPE: DNA
                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 2000-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/225,758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                         CDS
(19791)...(19802)
CDS
(21160)...(21370)
                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTAGATCCCAGCTCCTTCAGCTCCATGTCTGGTATATATGGGCAAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAAAAACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGAAAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTCACAACTTTCCTGGTCCTCTGGCTTTGGTCCTTCTTTCCTCCCTCCCTTCCCGTCCC 4197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATACACGGACTCCCTTCTGTGGACCCGTTTGGAGAGTCCAGAAGACTTTATCAATCCAC 460
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Pred. No. 1.9;
0; Mismatches 160; Indels

    See File Wrapper or

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1.9;
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; NAME/KEY: CDS
; LOCATION: (27235)...(27246)
US-09-800-631-96
                                                       RESULT 14
US-10-123-155-210/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/105.637
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 7
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Best Local S
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APPLICANT: Morris, David
APPLICANT: Engelhard, E:
Sequence 210, Application US/10123155 Publication No. US20030068794A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 63720
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Best Local Similarity
Matches 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN TITLE OF INVENTION: ASSOCIATED WITH ALTERED EXPRESSIC FILE REFERENCE: 529452500120
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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LOCATION: (24168)...
NAME/KEY: CDS
                                                                                                                                     38585
                                                                                                                                                                                                                                                                                        13340 CTTTCTCCTTGTCTGTGTCCTCTCCCTCTTCCATTTTCTCTTTGTTCTCTCCCCCCCACCT
                                                                                                                                                                                                                                                       326
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                                                                                                                                                                     GCCGCCTCGAATGCAGATACAC 407
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                                                                                                                                   ACTTCCTGTGTCTCACATGCAC 38606
                                                                                                                                                                                                                CTCCGCCACCCCACCCCTCTTCTCCCCTCTGTACTTGTCCCTGCCTTTTCCTCTCT
                                                                                                                                                                                                                                                   CTTTTTCACTCTGAGCAGTCTCCAGTTCCTCTGCTACCTTTTTGTCCTCCAAGCTTCCCT
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52.8%;
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Pred. No. 8;
0; Mismatches
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Pred. No. 5
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RESULT 9
US-09-934-455-17/c
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; LOCATION: (397)...(2457)
; OTHER INFORMATION: G877
US-10-295-403-75
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PRIOR FILLING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR FILLING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/113,409
PRIOR FILLING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 170
                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09934455 Publication No. US20030121070A1
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                                                                                                                                                                   PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                   PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR EILING DATE: 2001-04-17
                                                                                                                                                                                                                                                              FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant Traits
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NAME/KEY: CDS
LOCATION: (397)..(2460)
OTHER INFORMATION: G877
                                                                                                           LENGTH:
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                                                                         ORGANISM: Arabidopsis thaliana
                                                         FEATURE:
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                                                                                                               2603
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Similarity 62.5%;
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Jiang, Cai-Zhong
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Ratcliffe, Olive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keddie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Creelman,
                                                                                                                                                                                                                                                                                                                                                                                                  Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                    Riechmann, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                    Reuber, Lynne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert
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Pred. No. 1.1;
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Sequence 547, Application US/10205428

Publication No. US20030108907A1

GENERAL INFORMATION:
APPLICANV: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PA117C1
CURRENT APPLICATION NUMBER: US/10/205,428
CURRENT FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
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US-09-764-891-6229
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Publication No. US20030077808A1
GEMERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
CUGRENT APPLICATION NUMBER: US/09/764,891
CUGRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6229
LENGTH: 6146
TYPE: DNA
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Best Local S
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Pred. No. 1.9;
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Pred. No. 1.1;
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US-10-198-846-7264
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CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEO ID NOS: 14084
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7264
LENGTH: 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
           NAME/KEY: misc_feature
LOCATION: 819, 820, 821, 8
LOCATION: 840, 841, 842, 8
LOCATION: 865, 868, 869, 8
COTHER INFORMATION: n = A,T
                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 280, 324, 379, 3
LOCATION: 433, 445, 458, 4
LOCATION: 529, 533, 540, 5
LOCATION: 617, 623, 624, 6
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Sequence 7205, Application US/09764891
publication No. US20030077808A1
GENERAL INFORMATION:
ITILE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 10231
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Best Local Similarity
"~*~hes 76; Conserve
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; Sequence 75, Application US/10295403
; Publication No. US20030101481A1
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SEQ ID NO 7205
LENGTH: 9743
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Best Local :
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                APPLICANT:
APPLICANT: Keddie, James
APPLICANT: Zhang, James
APPLICANT: Zhang, James
APPLICANT: Benito, Maria-Ines
APPLICANT: Yu, Guo-Liang
APPLICANT: Fromm, Mike
TITLE OF INVENTION: PLANT GENE SEQUENCES I
FILE REFERENCE: MBI-0003
CURRENT APPLICATION NUMBER: US/10/295,403
                                                                                                                                                                                                                APPLICANT: Heard, APPLICANT: Riechr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                               Pineda, Omaira
Reuber, Lynne
Jiang, Cai-Zhong
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Adam, Luc
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Pred. No. 0.32;
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; SOFTWARE: FastSEQ f
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORCANISM: Human
US-09-759-359A-3
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US-09-759-359A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ABU-THREIDEH, Jane et al TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/759,359A CURRENT FILING DATE; 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                            497
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  TCCTTTTATGTCTTCCACCCCCACCCTTTCCCCTCCCTGCCCTC 628
                                                                                                                             CACGGACTCCCTTCTGTGGACCCGTTTGGAGAGTCCAGAAGACTTTATCAATCCACTTTT
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                                                                                     GAATCACGAATGCCCTGAGGTGCACAGCCCCTTTCCCCCTCTTTCGCGTCCTGAAGGGGTT
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Pred. No. 0.63;
0; Mismatches 191;
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Query Match
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Score

36.2;

ВВ 9

Length 1714;

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RESULT 5
US-10-242-056-60/c
; Sequence 60, Appl
; Publication No. U
; TOPOLOGY: 1; MOLECULE TYPE: US-10-242-056-60
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APPLICANT: Ensign
                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08
FILING DATE: 28-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
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COMPUTER READABLE FORM:
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APPLICANT: Rocheleau, Thomas A
TITLE OF INVENTION: Insecticidal
TITLE OF INVENTION: Photorhabdus
NUMBER OF SEQUENCES: 88
                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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APPLICATION NUMBER: 18-MAY-FILING DATE: 18-MAY-PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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CITY: Indianapolis
                                                  TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                      NAME: Borucki, Andrea T
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                              FILING DATE: 28-AUG-1996
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                                                                                   LENGTH:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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9330 Zionsville Road
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Petell, James
Fatig, Raymond
Schoonover, Sue
ffrench-Constant, I
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VENTION: Insecticidal Protein Toxins from
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                                    linear
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                DNA (genomic)
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US-10-184-634-120/c
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                                                                                                                                                                                                                                                             Query Match
Best Local
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 120
LENGTH: 1141
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Publication No. US20030068684A1
                                                                                                                                                                                                                                           Matches
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                 LENGTH: 1141
TYPE: PRT
ORGANISM: Homo Sapien
-10-184-634-120
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: 2hang, 2emin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
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                                                                                                                                                                                                                                       h 5.4%; Score 40.6; DB Similarity 11.0%; Pred. No. 0.011; 53; Conservative 145; Mismatches 2
                                                                                                                              CTAGAAACAGGGCTGTGGGGGGGGGGAGCCAACTTGGATCTGCCCCTTCTGAGGACACCTC
                                                                                                                                                             SC.AY.S.C.NSBAB.RMBMSCBHY.S.KTY.CYBBCS.....TKCT.S.....BYT
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                                                                                           YTSB.D....S.AT....B...AA..S.CSAS...R.AB.TCYMK.NC..G.BDSTN.NS
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               G..M.T.H.TYBCSRD.SH..KB...T.DTHHCHT...T.HS..NABK...C.B..CS.
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Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe, Colin K. Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, Victoria
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US-10-123-155-144/c
US-10-123-155-144/c
; Sequence 144, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
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Matches 49; Conserv
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CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C30
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                                                                                                               485
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AGCTTCCCTGCCGCCTCGAATGCACATACACGGACTCCCTTCTGTGGACCCCGTTTGGAGA 436
                                     ....TTH.DY..CCTYG....CWB.M.CY.YWGYCCM..R.HCHN.SBTTT..N...CBW
                                                                        ACTTTGCTACTTTTCACTCTGAGCAGTCTCCAGTTCCTGCTACCTTTTTTGTCCTCCA
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Sequence 124, App
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Sequence 7205, App
Sequence 75, Appl
Sequence 17, Appl
Sequence 629, Appl
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•	Sequence 3, Appli	w	Sequence 2520, Ap	σ	Ø	Ø	6.4	Sequence 10, Appl	676	54,	Sequence 53, Appl	e 91,	ce 499	e 51,	e 49,	Sequence 47, Appl	584	4	30, Ap		e 316,	e 1456	30	e 150	e 3, Aj	Sequence 554, App

## ALIGNMENTS

; TYPE: PRT ; ORGANISM: Homo Sapien US-10-184-644-120 RESULT 1 US-10-184-644-120/c 20 Prior Application removed NUMBER OF SEQ ID NOS: 612
SEQ ID NO 120
LENGTH: 1141
TYPE: PRT Sequence 120, Application US/10184644 Publication No. US20030044930A1 Query Match
Best Local Similarity
Matches 53; Conserv APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian INFORMATION: 862 SC.AY.S.C.NSBAB.RMBMSCBHY.S.KTY.CYBBCS.....TKCT.S.....BYT 803 142 CCTGTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTGTTTCTTGACTTGCT 201 262 TGGTGCTGCCTGGCCCAGGTCTCCTGTGTGTTTCTCTCTGAGCCGATG--CCTTTGACT 319 YTSB.D....S.AT....B...AA..S.CSAS...R.AB.TCYMK.NC..G.BDSTN.NS CTAGAAACAGGGCTGTGGGGGTGGGGAAGCAACTTGGATCTGCCCCTTCTGAGGACACCTC 261 Smith, Victoria Watanabe, Colin K. Wood, William I. Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Pan, James Desnoyers, Luc Conservative 5.4%; Score 40.6; DB 9; 11.0%; Pred. No. 0.011; vative 145; Mismatches 281; See File Wrapper or Palm 281; Length 1141; Indels Gaps . 743 1;

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
COMPUTER: IBM compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: WOR'D 97 (DOS text format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,584A
FILING DATE: 04-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026.9180
TELECOMMUNICATION INFORMATION:
TELEPAN: (608) 257-2501
TELEPAN: (608) 257-2275
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 bp
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Clicular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
IMMEDIATE SOURCE:
LIBRARY: plasmid, pGem3Zf(+)
CLONE: G210
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 8p
US-09-018-584A-19
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Search completed: July 8, 2003, 05:55:08 Job time: 198.615 secs
                                                                                                                                                                                                                                             Query Match 4.2%; Score 31.4; DB 4; Length 444; Best Local Similarity 64.4%; Pred. No. 2.2; Matches 47; Conservative 0; Mismatches 26; Indels
                                                                                                                                                              395 AAAAACAATGTCT 407
                                                                                                          644 AAAAACAAGTTCT 656
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Best Local Similarity
"~+~hes 51; Conserv
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; UNITS: bp
US-08-785-420-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09007005B Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER FILING DATE: 1997-01-27 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 57-5102
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                            TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Porcine RYR1 Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: Sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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     151
                                                                                                                                                                   461 TITTITTTCTTTTCATTTGGCCCTGGGGGCCGACGGTTAAGTACTTTATTCTGTCATTC 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 GTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAGATACACGGACTCC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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YCYGYTYTYAYCYGYCYAYGYCYAYGYGYTYCYTYTYCYTYTYCYAYGYAYGYAYTYC 92
                                  TGTCGAATCACGAATGCCCTGAGGTGCACAGCCCCTTTCCCCTCTTTCGCGTCCTGAAGG 580
                                                                                                                                     TTTTTTTTTTTTTTTTTTTTTTAYGYCYGYCYAYAYGYAYGYTYTYAYCYGYCYAYGYC
                                                                  YTYGYTYTYCYCYAYGYTYTYTYGYTYGYTYTYTYCYAYGYCYTYGYTYTYCYAYCYGYA 152
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56.6%;
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                                                                                                                                                                                                                         Score 31.8;
Pred. No. 1
                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                         97;
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RESULT 15
US-09-018-584A-19
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US-09-244-796-3/c
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CURRENT APPLICATION NUMBER: US/09/244,796

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/035,963

EARLIER FILING DATE: 1997-01-27

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                               Sequence 19, Application US/09018584A Patent No. 6238863
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09244796 Patent No. 6281344
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APPLICANT: Roberts, Richard W.
APPLICANT: Riche
TITLE OF INVENTION: SELECTION OF PROTEINS USING
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 277
                                                                       NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Promega Corporation
STREET: 2800 Woods Hollow Road
                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                          APPLICANT: Schumm, APPLICANT: Bacher,
                                                                                                                                                                  TITLE OF INVENTION:
STATE: Wisconsin COUNTRY: U.S.A. ZIP: 53711-5399
                                                      STREET: 2800 v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 TITTTTTTTTTTTTTTTTTTAYGYCYGYCYAYAYGYAYGYTYTYAYCYGYCYAYGYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 YTYGYTYTYCYCYAYGYTYTYTYGYTYGYTYTYTYCYAYGYCYTYGYTYTYCYAYCYGYA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 TTTTTTTTCTTTTCATTTGGCCCTGGGGGCCGACGGTTAAGTACTTTATTCTGTCATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAAAAAACAAGTTCTCTAAACGTTTTCGATGT 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCGAATCACGAATGCCCTGAGGTGCACAGCCCCTTTCCCCCTCTTTCGCGTCCTGAAGG 580
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                                                                                                                                                                                                                          Jeffery W.
                                                                                                                                                             MATERIALS AND METHODS IDENTIFYING AND ANALY! REPEAT DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.2%; Score 31.8; [
23.9%; Pred. No. 1.3;
tive 65; Mismatches
                                                                                                                                                                                 ETHODS FOR ANALYZING
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                                                                                                                                                                                     INTERMEDIATE TANDEM
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LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-072-596-323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-921-195-1/c
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08921195
patent No. 6147052
GENERAL INFORMATION:
APPLICANT: CHAU, RAYMOND M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 102;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ISOLATION AND USE OF ERYTHROID TITLE OF INVENTION: DIFFERENTIATION AND DENUCLEATION FACTORS NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                         STREET: 633 WEST S:
CITY: LOS ANGELES
STATE: CA
COUNTRY: USA
ZIP: 90071
                                   APPLICATION NUMBER: US/08/921,195 FILING DATE: 29-AUG-1997
                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTCTNYCTCWCKACGTYCKCCKCTMCKCNYMCNRWCTYRCCTCKKCCNCCRNCKNMCMK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTATTCTGTCATTCTGTCGAATCACGAATGCCCTGAGGTGCACAGCCCCTTTCCCCCTCT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCWCTCTCWCTYATCTCKCTCWCNYCMYMKMCACNCKCYAYTCNACTMNMWNCCANCNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCGAATGCAGATACACGGACTCCCTTCTGTGGACCCGTTTGGAGAGTCCAGAAGACTT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCACTKMKCCKMTCTCCTTMCKCCYMWCNTCCMKYNCCCTCCNMTCMTCKYTCCTCNCN 847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCMNMCWCMTCWCTWNAKCANCNTTCTTCTCTCMMYMTMACKCWCNNTCNCCKSGACCYT 787
                                                                                                                                                                                                                                                                           E: LYON & LYON 633 WEST SIXTH ST.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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27.1%; Pre
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                             SUITE
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Best Local
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                                                                                                                                                                                                                                   FILING DATE:
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TELEFAX: 213-955-0440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2721 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,923
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213,489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2721 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                  1474 TATEGOTCCAGTCCAGETTACTTTCCTGACCTCCAAGTCTCCCTTTTCACCTGEGGATTT 1415
                                                                                                                                                                                                                                                                                              282 CTCCTGTGTGTTCTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCTGAGC
                                                                                                                                                                                                                                                                                                                                         l Similarity
93; Conserv
                                                                                 CCACCTGGAGCCCGGCCAGCCTCACTCCCTGCAGGTCCAAGCAGAACTTGGCTACCTCCT 1355
                                                                                                                                                                                                           AGTCTCCAGTTCCTCTGCTACCTTTTTGTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAG
GTATCCGCTTTTCC 1341
                                                                                                                                                                                                                                                     CTCCTGGGTGATTTCACCTACACGCTGAGCCTCTGTCTCTGAGCCACTGACACCTAAACC
                                    TTTTTTTCTTTTTC 475
                                                                                                                       ATACACGGACTCCCTTCTGTGGACCCGTTTGGAGAGTCCAGAAGACTTTATCAATCCACT
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                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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Pred. No. 2.9;
0; Mismatches 101;
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                                                                                                                         461
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                                                                                                                                                                                                                                                                                                341
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AFFLING DATE:
FILING DATE:
APPLICATION NUMBER: US 08/030,159
FILING DATE: 15-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: LAYTON,UT., Samuel G.
REGISTRATION NUMBER: 22807
REFERENCE/DOCKET NUMBER: 3477-73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-377-1561 Sequence 1, Application US/08785420 Patent No. 6001976 GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: NUMBER OF SEQUENCES: 3 APPLICANT: MacLennan, David H
APPLICANT: O'Brien, Peter J.
TITLE OF INVENTION: DIAGNOSIS FOR
TITLE OF INVENTION: HYPERTHERMIA APPLICATION NUMBER: CITY: Charlotte, STATE: No. 6001976th Carolina 28234 COUNTRY: U.S.A. CLASSIFICATION: ADDRESSEE: B Bell, ell, Seltzer, Drawer 34009 Peter J.
DIAGNOSIS FOR PORCINE MALIGNANT US/08/785,420 08/249,388 Park & Gibson

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GENERAL INFORMATION:
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TOPOLOGY: lin
MOLECULE TYPE:
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LENGTH: 2478 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BUCCA Ph.D., Daniel
REGISTRATION NUMBER: 42,368
REFERENCE/DOCKET NUMBER: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-756-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                       FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floopy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/485,355B

APPLICATION NUMBER: US/08/485,355B
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Christian TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2117 GGCGAAGGCAGAAACGGCGGCGCGAAGTTGTCAGTGGCGGGGTAGACACCTGTGAGACG 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2057 GGTGGCCAGGTCGTCGGCGAGGCAGGATCTCCTCATTCTTG 2015
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APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Christian, P. D., Gordon, K. H.J., Han:
NVENTION: Insect Viruses and Their Uses
Protecting Plants
                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
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Pred. No. 1
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US-09-072-596-323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Best Local Similarity 50.3%;
Matches 82; Conservative
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REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 398-3249
TELEPHONE: (415) 398-3249
TELESTICS: 10 277299
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS: LENGTH: 2479 harm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                  ZIP: 98104-/--
ZIP: 98104-/--
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: TBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPUTER: PC-10S/MS-DOS
APPLICATION NUMBER: US/0
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 283..2307
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-AUG-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2058 GGTGGCCAGGTCGTCGGCGAGGCAGAGGATCTCCTCATTCTTG 2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2118 GGCGAAGGCAGAAACGGCGGCCGCGAAGTTGTCAGTGGCGGGGTAGACACCTGTGAGACG 2059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323, Appl
o. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 AAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGCTGAGCACGTGGAGTTAGG 84
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2479 base pairs TYPE: nucleic acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                      Washington
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                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09072596
                                                                                                                                                                                                                                       USA
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Dillon, Davin C.
Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                      Hendrickson, Ronald C.
ENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                             Twardzik, Daniel R. Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghton, Raymond
Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                               SEED and BERRY LLP
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                                                                           US/09/072,596
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RESULY: ,

US-08-48:335B-49/c

; Sequence 49, Application US/08485355B
; Sequence 49, Application US/08485355B
; Patent NO. 6177075
; GENERAL INFORMATION: Insect Viruses and Their Uses in

"""" OF INVENTION: Insect Viruses and Their Uses in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 283.753; SEQUENCE DESCRIPTION: SEQ ID NO: 47: US-08-485-3558-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION UNMEER: U$/08/485,355B

FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: U$ 08/440,522

FILING DATE: 12-MAY-1995

APPLICATION NUMBER: U$ 08/089,372

FILING DATE: 08-JUL-1993

APPLICATION NUMBER: AU PL4081/92

FILING DATE: 14-AUG-1992

ATTORNEY/AGENT INFORMATION:

NUMBER: TYPORMATION:
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REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                            2117 GCCGAAGGCAGAAACGGCGGCCGCGAAGTTGTCAGTGGCGGGGTAGACACCTGTGAGACG 2058
                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                 145
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82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGTTAGGGGACTCGGAGACTGCGATGCTGCCAGGAAAAGGGTGGAGCGGGTGAGTGCCT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGGACTTGATGATGGAGGACGTTGCCTCCGACTTCAGCACGGAGGACAGCATGTTCGC
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                       GGTGGCCAGGTCGTCGGCGAGGCAGGATCTCCTCATTCTTG 2015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: unknown
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50.3%;
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NAME/KEY: CDS;
; LOCATION: 366..2306
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-485-355B-49
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                                                                                                                                                                                                                                  Sequence 1, Application US/09194613 Patent No. 6251654 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2478 base pairs
                                                                                            APPLICANT: GORDON, Karl H.
APPLICANT: HANZLIK, Terry N.
TITLE OF INVENTION: MODIFIED SMALL RNA VIRUSES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: MCDermott, Will & Emery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                                     STREET: 600 15...
CITY: Washington
COUNTRY: USA
ZIP: 20005-3096
                                        STATE: D.C
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REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELECPHONE: (415) 781-1989
TELECAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2177 AACGGACTTGATGATGGAGGACGTTGCCTCCGACTTCAGCACGGAGGACAGCATGTTCGC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: unknown
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                                                                                   600 13th Street, N.W.
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Pred. No. 1.
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2118

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APPLICANT: SOSTEK, Jack W.
APPLICANT: ROBERTS, RICHARD W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FSETSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
COCCANICM: Artificial Sequence
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US-09-007-005-17
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US-09-007-005-17/c
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Best Local S
Matches 36
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                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(289)
                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Translation template
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                                                                                                                                                                                                                                                          Local Similarity
les 36; Conserv
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SYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCYAYTYTYGYTY 45
                              TACCTTTTTGTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAGATACACGGACTCCCTTCT 419
                                                                                             CTGAGCCGATGCCTTTGACTTTGCTACTTTTCACTCTGAGCAGTCTCCAGTTCCTCTGC 359
                                                                                                                                                          TTTTTTTTTTTTTTTTTTTTTTAYGYCYGYCYAYAYGYAYGYTYTYAYCYGYCYAYGY 225
                                                                                                                                                                                                                        YYYYGTACCAAATTCTTCTATCTCTTT 1457
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                                                            CCAAAAACAAGTTCTCTAAACGTTTT 667
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Pred. No. 0.025;
7; Mismatches 149;
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                                                                                                                                                                                                                                                                                       Length 289;
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RESULT 6
US-08-485-355B-47/c
; Sequence 47, Application US/084
; Patent No. 6177075
; Patent INFORMATION:
APPLICANT: Christian, P
TITLE OF INVENTION:
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NAME/KEY: misc_feature

LOCATION: (1)...(289)

CHEER INFORMATION: n =

US-09-244-796-17
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US-09-244-796-17/c
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/044,491
EARLIER APPLICATION NUMBER: 60/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1997-01-14
EINTER FILING DATE: 1998-01-14
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 17
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 289
TYPE: RNA
ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 TATTITTGTTTGTTGACTTGCTCTAGAAACAGGGCTGTGGGGGTGGGGAAGCAACTTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 TCTGCCCTTCTGAGGACACCTCTGGTGCTGCCTGGCCCAGGTCTCCTGTGTGTTTCTCT
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36; Conserv
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12.8%;
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Pred. No. 0.025;
17; Mismatches 1
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OF INVENTION: Insect Viruses and Their Uses
Protecting Plants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:

Hanzlik,

419

359 165 299 225

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US/08485355B

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              Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Applicat GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                          APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
TOTAL CONTROL OF THE PRIOR APPLICATION DATA:
TOTAL CONTROL OF THE PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 base pairs
                                                                                                                                                  FILING DATE: 16-APR-1996 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 2887 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MOI
TITLE OF INVENTION: ANI
NUMBER OF SEQUENCES: 34
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-AUG-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                   APPLICATION NUMBER: IL 1 FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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ilarity 93.5%;
Conservative
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                             16.4%;
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              Score 123.6; DB 5;
Pred. No. 2.4e-29;
0; Mismatches 9;
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Pred. No. 2.4e-29;
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                                            Length 2887;
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             Gaps
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US-08-232-463-14
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                                                                                                                       Matches
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CITY: Alexandria
                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                       Local Similarity es 13; Conserv
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TELEFAX: (703)683-410
TELEX: 899149
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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341 CAGTCTCCAGTTCCTCTGCTACCTTTTTGTCCTCCAAGCTTCCCTGCCGCCTCGAATGCA 400
                                                                                                                                                                                                                                                                                     281 TCTCCTGTGTGGTTTCTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCTGAG
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                                                                                                                                                                                     GGGTGAGTGCCTGTTGCC 150
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1800 Diagonal Road,
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JMBER: EP 91 114 300.6
26-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                   11.1%; Score 83.8; DB 3.4%; Pred. No. 2e-16;
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                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 128;
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3: /cgn2_6/ptodata/1,
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1278.561 Million cell updates/sec
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PCT-US96-10521-14
US-08-232-463-17
US-09-244-796-17
US-09-485-355B-47
US-09-194-613-1
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US-09-072-596-323
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US-08-20-03A-1
US-09-18-096-10
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## ALIGNMENTS

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COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,502
FILING DATE: 16-CAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-UN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,615
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
                                                            APPLICATION NUMBER: IL 115,319
FILLING DATE: 14-SEP-995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 116,588
FILLING DATE: 27-DEC-995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILLING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE,DOCKET NUMBER: WAI
TELECOMMUNICATION INFORMATION:
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APPLICANT: Tanya M. GONCHAROV
APPLICANT: YUYY V. GOLTISEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION
TITLE OF INVENTION: AND OTHER PROTEINS
NUMBER OF SEQUENCES: 34
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STREET: 41
CITY: Wash
STATE: D.C
COUNTRY: U
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SYSTEM: PC-DOS/MS-DOS
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14-JUN-1996
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Search completed: July 8, 2003, 05:51:12 Job time : 5682.6 secs	704 CNYTCTGGCTYCYCCYCCCCGYCGGYCGGYCYCSYCCTTYCBGXKGGTTG 755	588 TITTATGTCTTCCACCCCACCCTTTCCCCTCCCTGCCCTCTGTTTTTGTTG 639	644 ***********************************

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Use of BAC end sequences from Trypanosoma brucei GUTat 10.1 RPCI-93 Library for gene discovery and sequence-ready map construction Unpublished (1999)-EcoRI-2HII.TV Contact: Najb M. El-Sayed Construction M. El-Sayed
                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           page: http://www.tigr.org/tdb/mdb/tbdb/
Seq primer: SP6
Class: BAC ends.
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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RPCI93-ECORI-2H11.TP RPCI93-ECORI
RPCI93-ECORI-2H11, DNA sequence.
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Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences search
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                                                             GTGATGGTGAAATCATCGACGCCCCTCCCTGCGCCCCTTTCTCCCCGTCTTCTGCGGCCTT
                                                                                                   CATTCTGTCGAATCACGAATGCCCTGAGGTGCACAGCCCCTTTCCCCCTCTTTCGCGTCCT 575
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/clone="RPC193-EOGRI-2H11"
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/clone="RPC193-EOGRI"
/clone="RPC193-EOGRI"
/constructed for The Institute for Genomic Research by
Bohui Zhao in Pieter de Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
brucei TREU927/4 GUTat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPC193-EOGRI segment) or Dpn II (RPC193-BDRII
segment). High molecular weight fragments were ligated in
pBACe3.6 vector digested with Eco RI or Bam H1,
respectively. The average insert size is 141 Kb. Total
coverage (both segments): > 90 X the haploid
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/strain="TREU927/4 GUTat 10.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                          TGTGGTTTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCTGAGCAGTCTC
                                                TYYYTYCCCCCCCCCCCCCYTCCCCTYTTTYCCTYSCYTGCCCGCTTTTYYTTYTYTCT
                                                                                                                                                  GGACTCCCTTCTGTGGACCCGTTTGGAGAGTCCAGAAGACTTTATCAATCCACTTTTTTT
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                                                                                                 TCTTTTTCATTTGGCCCTGGGGGCCGACGGTTAAGTACTTTATTCTGTCATTCTGTCGAA
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/organism="Drosophila m
/ob_xref="taxon:7227"
/clone="BACR18111"
/clone="lib="RPCI-98"
/note="end: TET3"
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segref@genoscope.cns.fr
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AL106993
AL106993.1
                                                                                                                                                                                                                               Submitted (23-JUL 1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS01607 1101 bp DNA linear GSS 20-JUL-13 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN16K04 of DrosBAC library from Drosophila melanogaster (fruit
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1 (bases 1 to 1101)
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                                                                              /organism="Drosophila
/db_xref="taxon:7227"
/clone="BACN16K04"
/clone_lib="DrosBAC"
                                       /plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                          Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fly), genomic survey sequence.
AL106691
AL106691.1 GI:5623268
GSS.
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Direct Submission
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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                ATMWCAAHMCWCYTTTTTMYWATTTYTMYMTTMCWYMYCHYTTMHTHTTYYYCYTYTTAT 1021
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                                                       CCAAAAAACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGGAAAATTAACCTGCACCC
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/plasmid="pBeloBAC11"
/note="end: SP6"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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AL514103
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Genoscope - Centre National de Sequencage
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/db_xref="taxon:9606"
/clone="cLOBA0052F03"
/clone=lb="LTI_NFL006_FL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; %
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/note-Tector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
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                                                                                                                                                                                           Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

S continuous description of Drosophila DNA Rosource Center can be location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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70 c 231 g 112 t 8
                                                                                       /clone="BACR14J21"
/clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email : fliang@lifetech.com URL
                                                                                                                                             /organism="Drosophila
/db_xref="taxon:7227"
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   <u>დ</u> თ
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                                                                        112
   Score 43.2;
Pred. No. 1
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                                                                                                                                                              melanogaster"
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                   Length 910;
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                                                                        others
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δÃ

BASE COUNT

Matches

Query Match Best Local .

0;

Gaps

0

969

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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95;
                                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fly), genomic survey sequence. AL108773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome sur BACN37P10 of DrosBAC library from
                                                                                                                                                                                                                                                                                                                                          Genoscope.
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                                                                     pBeloBAC11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
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/clone=lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
a 174 c 277 g 1
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/organism="Drosophila melanogaster
                                             Location/Qualifiers
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/db_xref="taxon:7227"
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Pred. No. 0.24;
95; Mismatches
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JOURNAL
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Best Local
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                                                                                           Submitted (02-JUN-1993) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1993) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DAN provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be rocarion/Onatifice.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence T7 end or bac: BACR24F06 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 1101)
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/clone="BACN37P10"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
a 364 c 197 g
                                 /organism="Drosophila melanogaster
                                                                                 Location/Qualifiers
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1.27;
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GSS 03-JUN-1999

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REFERENCE

JOURNAL TITLE SOURCE KEYWORDS VERSION ACCESSION

ORGANISM

COMMENT

FEATURES

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1 (bases 1 to 772)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Roest-Crollius, H., Jaillon, O., Brottier, P., Quetien Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetien Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide ana midratoviridis DNA sequence
                                                                Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                          Bouneau,L., Billault,A.,
Weissenbach,J.
                                                                                                                                                                                                                                                                                       2 (bases 1 to 772)
Roest-Crollius, H., C
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Tetraodon nigroviridis genome surve
253F18 of library G from Tetraodon
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                                                                                                                                                                       Genoscope
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP). http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                CNS017RP 1101 bp DNA linear GSS 26-JUL-1 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37J10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                    Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone_lib="G"
/note="Genoscope:
a 52 c 257;
                Location/Qualifiers
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Pred. No. 0.19;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BGGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruiffly.org?he BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequenc BACR12K22 of RPCI-98 library from Drosophila
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                                                                      TGGGGAAGCAACTTGGATCTGCCCTTCTGAGGACACCTCTGGTGCTGCCTGGCCCAGGTC
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(bases 1 to 997)
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/clone_lib="RPCI-98"
/note="end : TET3"
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/db_xref="taxon:7227"
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  Query Match
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                                                                                                                                                                                                               Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR09Clf of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL066537
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa: Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 987)
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                                                                                    /clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                    /clone="BACR09C16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                   Berlin-Charlottenburg, GERMA
Location/Qualifiers
                                                                                                                                                                                                                                          No s1 sequence available.
This clone (DKF7p686E18155) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd. Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 421)
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DKFZp686E18155_rl 686 (synonym: hlcc3) Homo
DKFZp686E18155 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Bloecker |
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                /note="Vector: pTriplEx2; Site_1:
cDNA-collection"
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/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
                                                                      /clone="DKFZp686E18155"
/clone=lib="686 (synonym: hlcc3)"
/tlssue_type="human skeletal muscle"
/dev_stage="adult"
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/db_xref="taxon:9606"
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                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                'lab_host="DH10B"
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73 CGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGATGGTGCCAGGAAAGGGTGGAGC
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High quality sequence stop: 620.
Location/Qualifiers
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Tissue Procurement: Life Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, N
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Mammalia; Eutheria;
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                                                                                                                                                             /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176548"
/clone_lib="NIH_MGC_115"
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd

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Run
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AL600571 DKFZp313F
AL702116 DKFZp686E
BI844550 603033156
AL060767 Drosophil
AL066537 Drosophil
AL190051 Tetraodon
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02143 Pa	4622 Drosophi	65856 Dr	43041 Pa	06697 Dr	20430 HS	74596 AG	96162 60	58373 AGENCOUR	63694 Drosophi	49911 SALK_030	56472 HVSMEnOC	72006 Drosophi	53904 L30-2344	98338 Drosophi	60213 Drosophi	32141 Tetraodo	84648 Pan trog	06141 Drosophi	74918 Drosophi	19154 L0921E07	29299 Pan troc	69107 Drosophi	16605 T7 end c	79653 015_G_08	9834 ta97bll.x	70988 Drosophi	278 T14C14-Sp6	483 F14G2-Sp6	97207 Drosophi	78250 Drosophi	46132 1	06691 Drosophi	06993 Drosophi	65629 Drosophi	4103 AL51410	68148 Drosop	08773 Drosophi	08415 Drosophi

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## 522 bp mRNA linear EST 14-AUG-2001 DKFZp313F1234\_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone DKFZp313F1234 5', mRNA sequence. AL600571.1 GI:15164077

ALIGNMENTS

REFERENCE AUTHORS TITLE COMMENT JOURNAL

SOURCE ORGANISM

Homo sapiens

KEYWORDS VERSION ACCESSION DEFINITION

EST

human.

RESULT 1 AL600571 LOCUS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 522)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S. EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.) Unpublished (1999) Contact: Ansorge W

No s1 sequence available. This clone (DKF2p313F1234) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5 sequence of the clone insert Clone from S. Wlemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de: sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. of the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene encoding a subunit of cellulose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA10594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA10594 standard; DNA; 10732 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7723 BP; 2272 A; 1681 C; 1868 G; 1902 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABB59675
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       n the
                                                                                                              2000-342371/30
)B; AAY85179.
encoding a cellulose synthetic equipment - amount of cellulose synthesised in a plant
                                                                                                                                                                                                                         MIZUNO K.
OJI PAPER CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTTTTTTCTTTT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGCCGTTGCTTCACCGGCGACAATATATTTGTTGAGAGTGGATTGCTTCTTGCCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATACACGGACTCCCTTCTGGGACCCGTTTGGAGAGTCCAGAAGACTTTATCAATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGTCTCCAGTTCCTCTGCTACCTTTTGTCCTCCAAGCTTCCCTGCCGCCTCGAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellulose production; increase
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Pred. No. 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10732 BP; 3149 A; 1212 C;
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                                                                                                                                 9150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                   CSDSTCCTTNCYDANCCYTCYTSTNCNSTCCYTTTDYSSRNSTSDYSNSTSTTBCTTSRT
                                                                                                                                                                                                                                                                                                  GCCGCCTCGAATGCAGATACACGGACTCCCTTCTGTGGACCCGTTTGGAGAGTCCAGAAG 445
                                                                                                                                                                                                                                                                                                                                                                       CTTTTTCACTCTGAGCAGTCTCCAGTTCCTCTGCTACCTTTTTGTCCTCCAAGCTTCCCT 385
                                                                                                                                                                                                                                                                                                                                                                                                       BYSNSTYDAYSSRYSCYTCYTCDYSSTCYTRCAKCTBCNSTSRAKSRTTTTTTYRCYCYT 9331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSCSRTBSRNSTCCCTBTTSRGNCCYDAYDANSTSRYDAYYDACYYSYDASTTBYSYSCT
AKYSTBCTTCTTSRSRRC
                                GCCCTCTGTTTTTGTTGC
                                                                YTTBDCYTNCNCAKSRGCSRTTRCSTSDTTTBCYTCCYRATBCYTNCNCTTCSTSTNCSR
                                                                                                TACTTTATTCTGTCATTCTGTCGAATCACGAATGCCCTGAGGTGCACAGCCCCTTTCCCC
                                                                                                                                                                                                                                                                     DCCYTCCNSTCYTCCSRCTBCYTTBCYRAYDAYSYDANSTSTSRCAKYSCCYTYSAKTTR
                                                                                                                                                                                                                                                                                                                                     SRCYTTBCYTCYTNCSRGCCSRTTSRSRYDAYSCNCNCSRSDYSTBCTTYDACYTCYTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGCCTGGCCCAGGTCTCCTGTGTGTGTTCTCTCTGAGCCGATGCCTTTGACTTTGCTA
                                                                                                                                 TCYTSRYSYDACYSNCCCTBAKCYTCSRCDCSRYSTTSRAKTBTTSTSDCYTNCCNCCCC
                                                                                                                                                                                                                                   ACT - - TTATCAATCCACTTTTTTTTTTTTTTTTTGGCCCTGGGGGCCGACGGTTAAG
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18.3%;
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9013
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Pred. No. 3.9;
67; Mismatches
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Search completed: July Job time: 755.255 secs 00

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RESULT 13
ABL03779/c
ID ABL03779;
XX ABL03779;
XX ABL03779;
XX ABL03779;
XX DE Co-MAR-2002 (first |
XX DE Drosophila melanogas:
XX Drosophila; developm
KW pharmaceutical; gene
CS Drosophila melanogas:
XX Pho Wo200171042-A2.
XX PD 27-SEP-2001.
XX PP 23-MAR-2001; 2001W0-1
XX PP 23-MAR-2000; 2000US-1
PR 23-MAR-2000; 2000US-1
PR 11-JUL-2000; 2000US-1
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25-0C1-1999
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28-0C1-1999
                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster expressed polynucleotide SEQ ID NO 5819
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08-OCT-1999;
                                                                                                                                                 23-MAR-2001; 2001WO-US09231
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                       Adams M,
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2000US-0614150
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99US-0161361.
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99US-0160741.
99US-0160767.
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99US-0159638.
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99US-0159330.
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99US-0161404
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-0160770
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                       Li PWD,
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RESULT 14

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ID ABL03

XX ABL03

AC ABL03

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WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID
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P-PSDB; ABB59676.
                                                   Venter JC, Adams M,
                                                                                                      (PEKE )
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11-JUL-2000;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun disorders -
           25-FEB-2000; 2000EP-0301439.
                              06-SEP-2000.
                                                                   Arabidopsis thaliana.
                                                                                       metabolic
                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                           Arabidopsis thaliana DNA fragment SEQ
                                                                                                                                                                 AAC36552;
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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18-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation.
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                                                                                     sequence; ss.
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/*tag= s
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RESULT 10
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                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
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                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                 nervous system
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26-FEB-2001; 2001WO-US04927.

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RESULT 8
ABL33323/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the genome, which encodes one or more messenger RNA splice variants.

Combined the oligonucleotide libraries are useful for detecting mRNAs from a complexical sample, in expression profiling studies, in qualitatively or complexity characterising the corresponding transcriptome, and in complex transcripts and splice variants of human or animal comparison. The libraries may also be used as specialised minical comparison to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the condition, to detect developmental specific genes such as those genes condition; to detect developmental specific pathological condition; to detect developmental specific pathological condition; to detect developmental specific pathological condition; to detect developmental specific genes; and to detect RNA confirmation aparticular disorder. ABN27253 to ABN39589 represent colligonucleotide sequences from rats, humans and mice, which are used in the sequence data for this patent did not form part of the printed constitution, but was obtained in electronic format directly from WIPO at the wine intention, but was obtained on sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              messenger RNAs that populate a (sub-)transcribed from multiple (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a several oligonucleotides, each capable of hybridising selectively to a several oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oligonuclectide libraries comprising oligonuclectides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000US-221607P. 02-MAY-2001; 2001US-287724P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental-specific genes
               Homo sapiens
                                                                                       antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                             antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                 ABL33323
                                                                      neurofibromatosis;
                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                    immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                         immune system disease; cytosine methylation; antiasthmatic; teriosclerotic; antianaemic; cytostatic; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60; Conser
                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGATGGTGCCAGGAAAGGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                         ACGTGGAGTTAGGCAGTTAGGGGACTCGGAGACTGCGATGGTGCCAGGAAAGGGTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВÞ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes oligonucleotide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                  system associated gene
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 A; 8 C;
                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              populate a (sub-)transcriptome, where the comprises messenger PNNo +----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 G; 10 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60;
Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                    SEQ ID NO: 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
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                                                                    epilepsy;
bowel disease;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A,
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                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                         Mouse; human; DNA polymerase lambda; DNA repair; isoform; neurodegenerative disease; gene therapy; pol kappa; POLL; aging; immunosuppression; psoriasis; arthritis; graft reje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-)
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                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine DNA polymerase lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH25711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH25711 standard;
                    intron
                                                                                                                                                                     intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention provides a number of human immune system associated
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67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTTTGCAAAATGAACTTTTTTTTTTTTGATCCTGTACACTGGTTTTTTAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAAAAAACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGAAAATTAACCTGCACC 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2000DE-1043826
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                  /*tag= c
/number= "2"
965..1624
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59..827
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828..964
                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2623 A; 195 C; 1863 G; 5060 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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ment of diseases associated
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                 graft rejection; ds
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RESULT 6
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; respiratory distress syndrome; protozoal infection; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymes involved in proteolytic cleavage. An expression cassette containing fusion polypeptide is used to identify a mutant cell line deficient in an enzyme of interest and is also useful for diagnosis and suppression of proliferation or metastases of a tumour cell characterised by overexpression of a polypeptide (e.g. Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA encoding fusion polypeptide is used in gene therapy.
                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                             diagnostic markers that drug toxicity -
                                                                                                                                                                                                                                                                                                                                                        Detecting granulocyte activation of genes associated with granuloc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beazer-Barclay Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             granulocyte activation; chronic inflammation; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK84723 standard; cDNA; 2887
invention relates to detecting (M1) granulocyte (GC) activation A), by detecting the level of expression of gene(s) (GS) identif chip analysis as given in the specification, and comparing expression level to an expression level in an unactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-435328/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGATTATATTCTCCTGCC 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGATGGTGCCAGGAAAGGGTGGAGC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGAGCA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentially expressed in granulocytic cells #1294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-237189P
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                                                                                                                                                                                                       No 1294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853 A; 595 C; 625 G; 814 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.4%;
93.5%;
                                                                                                                                                                                                                                                                                                          ctivation by detecting differential expression h granulocyte activation, which serves as is useful for monitoring disease states and
                                                                                                                                                                                          114pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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2.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vockley
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                                                                              (Gs) identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
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ARNSBULT 7
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XX Splix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chronic) in a tissue, an allergic response in a subject, exposure of a cohronic) in a tissue, an allergic response in a subject, exposure of a cc subject to a pathogen or sterile inflammatory disease using the cc subject to a pathogen or sterile inflammatory disease using the cc subject to a pathogen or sterile inflammatory disease, by detecting the cc level of expression in a sample of the tissue of gene(s) from Gs, where cc level of expression of the gene is indicative of inflammation; cc (4) treating (M5) an inflammation (especially chronic) or in a tissue, cc an allergic response in a subject, exposure of a subject to a pathogen cc inflammatory disease, by contacting a tissue having cc from Gs in the tissue. M1 is useful for screening an agent capable of modulating GA; M3 is useful for screening an agent capable of modulating GCA, m3 is useful for screening an agent capable of modulating GCA perferably in an inflammation in a tissue; M4 is useful for cresponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, and allergic creperfusion injury, ARDS, adult respiratory distress syndrome, cc parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present cof the sequence represents a gene differentially expressed in granulocytes. Cc of the printed specification, but was obtained in electronic cof the printed specification, but was obtained in electronic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                         ABN58902 standard; DNA; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening for an agent capable of modulating GCA or an inflammation (especial)
                                                                                                                                                                                                                                                                           15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTGAGTGCCTGTTGCC 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGGAGTTAGGCAGGTTAGGGGACTCGGAGGACTGCGATGGTGCCAGGAAAGGGTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATTATATTCTCCTGCC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGCTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 853 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 123.6;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G; 814
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9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263
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Human; splice mouse; rat; splice transcript; detection; variant; transcriptome; oligonucleotide 1: RNA transcript;

Human spliced transcript detection oligonucleotide SEQ

ID NO:31650.

Homo sapiens

WO200210449-A2

20-JUL-2001; 2001WO-IB01903

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AAT61396, and AAT61405-T61411 represent coding sequences for different classforms of MACH. MACH is a binding protein for the mediator of receptor contactity (MoRT-1) protein. MORT-1 binds to the FAS ligand receptor contactity (MoRT-1) protein. MORT-1 binds to the FAS ligand receptor contactity (MoRT-1) protein, and triggers part of the cell death contactions, and antibodies (Ab) against them are consequences, the encoded proteins, and antibodies (Ab) against them are used to modulate the effect of FAS-R ligand or TMF on cells that carry contact to modulate the effect of FAS-R ligand or TMF on cells that carry contact. The encoded proteins are mediators of the cell death pathway continued the contact of MORT-1 where increased cytotoxicity is required. To inhibit the ceffect of MORT-1, e.g. in cases of septic shock, graft rejection and contact the patitis, sequences encoding antisense molecules or ribozymes, or ab against the protein, are used. Compounds that inhibit MACH are cottentially useful for controlling MACH activity e.g. in cases of autoimmune disease, oligodendrocyte death in multiple sclerosis or also be used to isolate and characterise other proteins and receptors involved in expectation of controlling and for Ab production. The Ab can be used to purify the new proteins and for diagnosis of conditions involving abnormal function of controlling and for diagnosis of conditions involving abnormal function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1996;
16-JUL-1995;
17-AUG-1995;
14-SEP-1995;
27-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WEIN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boldin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-FEB-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WC9703998-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       v DNA encoding MACH protein that interacts with MORT-1 protein
mediate intracellular effects of FAS or TNF receptors, partic
c regulating apoptosis in tumours, virus-infected cells etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
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YEDA RES & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 116-117; 163pp; English.
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                     cloning of genes encoding proteins or enzymes involved in proteolytic cleavage. The invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage site flanked by sequences encoding two caspase subunits. A fusion polypeptide comprising a first and a second caspase subunit, separated by a cleavage
                                                                                                                                                                  The present sequence is a DNA encoding human Caspase-8 also known as MACH, FLICE and Mch5. Caspases are a family of cysteine proteases, that participate in the initiation and execution of appropriate construction of a pro-enzymes, activated by cleavage into a large and small subunit, occurring after specific aspartic acid residues within the pro-enzyme sequence. The present invention relates to a method for functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour; cathepsin B; urokinase; proliferation; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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14-AUG-2000;
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DB; AAE00605.
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      associated in nature,
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      is useful for cloning
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            AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For
                                                                                                                                                                       metastasis
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Best Local
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                    TGTACACTGGTTTTTTA 748
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TGTACACTGTTTTTTAA 24782
                                                                 GTGGATTCGTG----AATTTATCTGTATC--TTTGCAAAATGTA--TTTTTTCTTTTGTATG
                                                                                                                                   TGCCCTCCTGCCCTCTCTTGTT-----CCCCAAAGACAGTTCTCTAA--TGTTTTGAT
                                                                                                                                                                     TTCCCCTCCCTGCCCTCTGTTTTTGTTGCCCCAAAAAACAAGTTCTCTAAACGTTTTCGAT
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                                                                                                Conservative
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9.3e-152;
hes 42;
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AAK77217 standard; DNA; 45017 BP
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
116-MAR-2000;
117-MAR-2000;
119-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic
cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                           17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                    Human immune/haematopoietic antigen genomic sequence
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2000US-0179065.

2000US-0180628.

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                                                                                                                                                                                                                                                                                                       antigen; cancer;
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14 - SEP - 2000
21 - SEP - 2000
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                                                                                                                                                                    Query Match
Best Local Similarity
Matches 675; Conserv
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17 - NOV - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                    Sequence 43938 BP; 12772 A; 9656 C; 9206 G; 12304 T; 0 other;
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                                                                                                   24420
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 133
                                                                                                                                    13
GGGTGAGTGCCTGTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTGTTTCT
                                                                                                                   TATTGAAAGTAAAAGAAACTTCCTTCCTGGGAGCCTTTCCCACCCCCCTTCCCTGAGCA
                                CGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGATGGTGCCAGGAAAGGGTGGAGC
                                                 CGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGATGGTGCCAAGAAAGGGTGCGAGC
                                                                                                  TATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGCTGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
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2000US-0251988
2000US-0256719
2000US-0251479
2000US-0251856
2000US-0251868
2000US-0251869
2000US-0251989
2000US-0251989
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2000US-0249214

2000US-0249215

2000US-0249216

2000US-0249217

2000US-0249218

2000US-0249248

2000US-0249245

2000US-0249264

2000US-0249264

2000US-0249269

2000US-0249299

2000US-0249299

2000US-0250160

2000US-0250160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
                                                                                                                                                                                  70.4%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32028; 3071pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
                                                                                                                                                                  Score 529.8; DB 22;
pred. No. 9.2e-152;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Listing; English
                                                                                                                                                                     Indels
                                                                                                                                                                                                    Length
                                                                                                                                                                                                      43938
                                                                                                                                                                    20;
                                                                                                                                                                    Gaps
                                                                132
 192
                                                                                                                                    72
                                                                                                   24361
                                 24301
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01-SEP-2000 01-SEP-2000 01-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 15-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 20-CCT-2000 20-CC

2000US-0241786 2000US-0241787 2000US-02393081
2000US-0235131242
2000US-0231244
2000US-023131242
2000US-02314143
2000US-02314143
2000US-0231968
2000US-023398
2000US-023398
2000US-023399
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2000US-0233964
2000US-0233964
2000US-0233964
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2000US-02330837
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2000US-0241808 2000US-0241809 2000US-0244617 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246477 2000US-0246524 2000US-0246524 2000US-0246524 2000US-0246526 2000US-0246526 2000US-0246527 2000US-0246527 2000US-0246527 2000US-0246527 2000US-0246613 2000US-0246613 2000US-0246613 2000US-0246613 2000US-0246613 2000US-0246613 2000US-0246613 2000US-0246613 2000US-0249208 2000US-0249208 2000US-0249208 2000US-0249210 2000US-0249211 2000US-0249211

660 660

720

753

sequence

SEQ

NO:32028

antigen; cancer; H

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gene inactivation. Methylation PCR can be used to examine even minute CC amounts of patient material to demonsrate whether the CASP8 gene can mrNA and protein product. The promoter Region 1 sequence is clocated upstream (5') to exon 1, which is the alternatively-spliced 5' cC untranslated region (UTR) that is less commonly used. The promoter Region 2 sequence is located downstream (3') of exon 1 and upstream of CC exon 2, which is the more commonly used 5' UTR. The CASP8 gene has been compared to human chromosome 2q33-34. The methods are used to diagnose cor prognose cancer. Cancer is treated by administering a vector that care expresses a gene encoding functional CASP8 in cells. The cancer that is diagnosed or treated is a tumour in which a myc gene is amplified, colorectal carcinoma, or uterine cervical carcinoma, juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces caps and can be called non-induced apoptosis in cells containing an inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inactivation of a caspase-8 (CASPB) gene is determined by detecting a modification of CASPB genomic DNA that results in inactivation of the gene. CASPB, a cysteine protease, is part of the death inducing signaling complex (DISC) associated with the Fas receptor. CASPB is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASPB promoter region sequences, in particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising
     541 GAGGTGCACAGCCCCTTTCCCCTCTTTCGCGTCCTGAAGGGGTTTCCTTTTATGTCTTCC
                                                                                                                                                        481
                                                                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           753
                                                                                            GCCCTGGGGGCCGACGGTTAAGTACTTTATTCTGTCATTCTGTCGAATCACGAATGCCCT
                                                                                                                             GCCCTGGGGGCCGACGGTTAAGTACTTTATTCTGTCATTCTGTCGAATCACGAATGCCCT
                                                                                                                                                                                                                                                                 ACCTTTTTGTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAGATACACGGACTCCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCCGATGCCTTTGACTTTGCTACTTTTCACTCTGAGCAGTCTCCAGTTCCTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCCCTTCTGAGGACACCTCTGGTGCTGCCTGGCCCAGGTCTCCTGTGTGGTTTCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTTGTTTCTTGACTTGCTCTAGAAACAGGGCTGTGGGGGTGGGGAAGCAACTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTTTGTTTCACTTGACTTGCTCTAGAAACAGGGCTGTGGGGGTGGGGAAGCAACTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGGGTGGAGCGGGTGAGTGCCTGTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTGCTGAGCACGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGATGGTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTGCTGAGCACGTGGAGTTAGGCAGGTTAGGGGACTCGGAAGACTGCGATGGTGCCAGG
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                                                                                                                                                                                                           TGAGCCGATGCCTTTGACTTTTGCTACTTTTTCACTCTGAGCAGTTCTCCAGTTCCTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGGGTGGAGCGGGTGAGTGCCTGTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 140 A; 204 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97-98;
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                                                                                                                                                                                                                                                                                                                         GTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAGATACACGGACTCCCTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 753; DB 21; Length Pred. No. 2.3e-221; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 2
AAK77216/c
AAK77216 standard; DNA; 43938 BP
XX
AX
AX77216;
XX
DT 07-NCV-2001 (first entry)
XX
DE Human immune/haematopoietic anti
XX
Human immune/haematopoietic; i
XW
Cytostatic; gene therapy; vaccin
XX
PN W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PPN W0200157182-A2.
XX
PPN W0200157182-A2.
XX
PPN W0200157000; 2000US-0198034.
PR 11-JAN-2000; 2000US-018663.
PR 24-FEB-2000; 2000US-018663.
PR 11-MAR-2000; 2000US-018663.
PR 11-MAR-2000; 2000US-0198123.
PR 11-MAR-2000; 2000US-0198123.
PR 11-MAR-2000; 2000US-0198123.
PR 11-MAR-2000; 2000US-0198123.
PR 11-JUL-2000; 2000US-0198123.
PR 11-JUL-2000; 2000US-020465.
PR 28-JUL-2000; 2000US-0216880.
PR 21-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-022526.
PR 11-JUL-2000; 2000US-022527.
PR 11-JUL-2000; 2000US-02252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCCCACCCTTTCCCCTCCCTGCCTCTGTTTTTGTTGCCCAAAAAACAAGTTCTCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; vaccine; metastasis;
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В δÃ В Qy В δÃ

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Вb

γ Вb QΥ В Ωy 밁 δÃ 뮍 δÃ

В

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                    529
529
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                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
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                                                                                                                      Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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753
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                         100.0
70.4
70.4
16.4
16.4
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## ALIGNMENTS

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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces
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                                                                                                          Quality coverage: 4.3 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 135267 bases at least Q30 Consensus quality: 142022 bases at least Q30 Consensus quality: 143507 bases at least Q20 Consensus quality: 143507 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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* 50640 50639; gap of 100 bp

* 50640 59088; contig of 8449 bp in length

* 59089 5188; gap of 100 bp

59189 5618; gap of 100 bp

66917 67011; gap of 1708 bp in length

67017 80823; contig of 13807 bp in length

80824 80923; gap of 100 bp

80924 99512; contig of 13807 bp in length

99513 99612; gap of 100 bp

99613 99612; gap of 100 bp
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2252 2351: gap of 100 bp
2352 4586: contig of 2235 bp in length
4587 4686: gap of 100 bp
4687 7924: contig of 3238 bp in length
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                                                                                                                                                         Submitted (20-JUL-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA on Jul 20, 2002 this sequence replaced gi:20270143.

* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Oryzeae; Oryzea; Oryzeae; Oryzea; Oryzea
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                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-MAR-2002) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 146383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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96; Conservative
                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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11884 GTAGTAAACAAAATGATTTATGTTTTCATGTTTATTTTGTATAATCTCAAGATGCATATT
                           636 GTTGCCCAAAAAACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGAAAATTAACCTG
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                                                       GAAAATGTTTCTATTTATTTCTGTAACTATCAATCTTTCTGTTACCTGGCTGCTTTGATA
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94933: contig of 43532 bp in length
94977: gap of unknown length
97166: contig of 2189 bp in length
97210: gap of unknown length
116754: contig of 19544 bp in length
116798: gap of unknown length
116383: contig of 29585 bp in length.
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2; Mismatches 92; Indels 0
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Unpublished
(bases 1 to 128941)
(bases 1 to 128941)
Worley,K.C.
Direct Submission
Submitted (11-FEB-2002) Human Genome Sequencing Center, Department Submitted (11-FEB-2002) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-701-2002) Human Genome Sequencing Center, Depoing Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18847091.

Center: Baylor College of Medicine Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
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Center clone name: CH230-25786

Center clone name: CH230-25786

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of rea Assembly program: Phrap; version 0.990329

Consensus quality: 84896 bases at least Q40
Consensus quality: 89166 bases at least Q30
Consensus quality: 92809 bases at least Q20
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 TCTCCTGTGTGTTTCTCTCTGAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCTGAG 340
                                                                                  Submitted (10-MAY-2001) Medicine and Biosystemic Science, Kyushu University Graduate School of Medical Science, 3-1-1 Maidashi, Higashi-ku, Fukuoka 812-8582, Japan
                                                                                                                                    Himeji,D., Tsukamoto,H. and Horiuchi,T. Direct Submission
                                                                                                                                                                                                               Characterization of caspase-8L: a novel isoform of behaves as an inhibitor of the caspase cascade Blood 99 (11), 4070-4078 (2002)
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1723)
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens caspase-8L mRNA, AF380342
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                                                                                                                                                                                                                                                                              Hime
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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/cell_type="peripheral blood lymphocyte"
86. .916
                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.4
                                                                                                                                                                                                                                                                         Tsukamoto,H.,
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, complete cds
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Best Local
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan;U., King,L., Korvah,J., Kovar,C.,
Karlsson,E., Kelly,S., Khan;U., King,L., Korvah,J., Louiseged,H.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonakke,T., Sparks,A., Stanley,H., Stone,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chaoko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, C., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hadraco, A., Honnes, M., Holloway, C., Hollows, C., Hollows
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Rattus norvegicus
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/protein_id="AAK57437.1"
/protein_id="AAK57437.1"
/db_xref="G1:14211398"
/translation="MDFSRNLYDIGEQLDSEDLASLKFLSLDYIPQRKQEPIKDALML
FQRLQEKRMLEESNLSFLKELLFRINRLDLLITYLNTRKEEMERELQTPGRAQISAYR
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9271594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane Research & Biophysics, Rehovot 76100, ISRAEL 4 (bases 1 to 2887)
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3 (bases 1 to 2887)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/product="MACH-alpha-1"
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FORLOGEKRULDESNLSSFLKELLFRINGLLDIFIEMERUPICGEKUDIL
KRYCAQINKSLLKIINDYEEFSXERSSSLEGSPDEFSNGEELGGYMTISDSPREQDSE
SQTLDKYYQMKSKPROYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTTTFEE
LHFEIKPHDDCTVEQIYEILKTYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAPIY
ELTSGFTGLKOPSLAGKFKYRETIQACGGDYQKGIPVETDSEEQPYLEMDLSSPQTRY
IPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILITEVNYEV
SSTEDKKNMGKQMPQPTTLKKKLYFSD"
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/note="triggers cell
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 777)
Breckenridge_D.G., Nguyen,M., Kuppig,S.,
The procaspase-8 isoform, procaspase-8L,
complex at the endoplasmic reticulum
Proc. Natl. Acad. Sci. U.S.A. 99 (7), 433
                                                                                                         I66494
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777 bp mRNA linear PRI 03-APR-2002
Homo sapiens clone 4 procaspase-8 (CASP8) mRNA, partial cds;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FQRLQEKRMLEESNLSFLKELLFRINRLDLLITYLNTRKEEMERELQTPGRAQISAYR
VMLYQISEEVSRSELRSFKFLLQEEISKCKLDDDMNLLDIFIEMEKRVILGEGKLDIL
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/protein_id="AAL87632.1"
/db_xref="GI:19401530"
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266. .>777
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/db_xref="taxon:9606"
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Breckenridge, D.G., Nguyen, M., Kuppig, S., Reth, M. and Shore, G.C
                                                                                                                                                                               1 (bases 1 to 2887)
Wallach,D., Boldin,M., Goncharov,T. and Golstev,Y.V.
Wadulators of the function of FAS receptors and other proteins
Patent: US 6399327-A 14 04-JUN-2002;
                                                                                                                                                                                                                                                                                                                                   Sequence 14 from patent US 6399327. AR211527
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ELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAPI
YELTSQFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPVETDSEEQPYLEMDLSSPQTR
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RVMLYQISEEVSRSELRSFKFLLQEEISKCKLDDDMNLLDIFIEMEKRVILGEGKLDI
LKRVCAQINKSLLKIINDYEEFSKERSSSLEGSPDEFSNGEELCGVMTISDSPREQDS
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/product="procaspase=8L"
/protein_id="AAL87628_1"
/db_xref="Gi:19401519"
/translation="MEGGRRARVVIESRRNFFLGAFPTPFPAEHVELGRLGDSETAMV
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PGKGGADYILLPFKKMDFSRNLYDIGEOLDSEDLASLKFLSLDYIPOJKQEPIKDALM
PGKGGADYILLPFKKMDFSRNLYDIGEOLDSEDLASLKFLSLDYIPOJKQEPIKDALM
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1. .2887
                                                                                                               /organism="unknown"
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/db_xref="taxon:9606"
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0; Mismatches 9;
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Pred. No. 4.3e-27;
0; Mismatches 9;
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HSMACHA1 2887 bp
H.sapiens mRNA for MACH-alpha-1
X98172
X98172.1 GI:1403318
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1 (bases 1 to 2887)

Cordell,B. and Li,Y.

Functional Cloning of genes encoding proteins/enzymes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteolytic cleavage Patent: WO 0129232-A Scios Inc. (US)
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15 from Patent WO0129232.
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ELTSQFTGLKCPSLAGKPKVFFIQACQCDNYQKGIPVETDSEEQPYLEMDLSSPQTRY
IPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVNYEV
SNKDDKKNMGKQMPQPTFTLRKKLVFESD"
3 595 c 625 g 814 t
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/translation="MDFSRNLYDIGEOLDSEDLASLKFLSLDYIPQRAQISAYR
FORLQEKRMLEESNLSFLKELLFRINRLDLLITYLNTRKEEMERELQTPGRAQISAYR
VMLYQISEEVSRSELRSFKFLLQEEISKCKLDDMLLDIFIEMEKRVILGEGKLDIL
KRVCAQIKKSLKIINVEEFFSKERSSSLEGSRDEFSNGEELCGVMTISOSPREQDSE
KRYCAQIKSLKIINVEEFFSKERSSSLEGSRDEFSNGEELCGVMTISOSPREQDSE
SQTLDKVYQMKSKPRGYYCLIINNHNFAKAREKYPKLHSIRDRNGTHLDAGALTTTFEE
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/db_xref="taxon:9606"
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93.5%;
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Pred. No. 4.3e-27;
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  2 (bases 1 to 982)
Teitz.f:, wei,T., Valentine,M.B.,
Valentine,V.A., Behm,F.G., Look,A.
Direct Submission
                                                             Teitz,T., Wei,T., Valentine,M.B., Vanin,E.F., Grenet,J., Valentine,V.A., Behm,F.G., Look,A.T., Lahti,J.M. and Kidd,V.. Caspase 8 is deleted or silenced preferentially in childhood neuroblastomas with amplification of MYCN Nat. Med. 6 (5), 529-535 (2000)
                                                                                                                 Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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Breckenridge, D.G., Nguyen, M., Kuppig, S., The procaspase-8L, complex at the endoplasmic reticulum proc. Natl. Acad. Sci. U.S.A. 99 (7), 43:
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Research Hospital, 332 N. Lauderdale, Memphis, TN 38105, USA
Location/Qualifiers
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/note="similar to E
(NID:g10991125)"
5615. .598"
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(NID:g10996436)"
5361. 5812
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/note="similar to I

(NID:g11617019)"

5237. .6019
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5551. .6327
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(NID:913283824)"
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(NID:g11047198)"
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91.6%;
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Pred. No. 3.9e-154;
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1622 TATTGAAAGTAGAAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGCTGAGCA
                13 TATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTTCCCTGAGCA 72
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 6502)
Hadano,S., Ikeda,J. and
Direct Submission
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Homo sapiens
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AB038981
AB038981.1 GI:12862688
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1744. .39
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/note="CDS is reported in
alternative 5'UTR"
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/db_xxef="taxon:9606"
/chromosome="2"
/map="2233"
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3971. .>6502
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for caspase-8,
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Pred. No. 3.8e-145;
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6 (bases 1 to 181150)
Waterston,R.H.
Direct Submission
Submitted (07-JUN-2001) Genome Se
University School of Medicine, 44
MO 63108, USA
7 (bases 1 to 181150)
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Submitted (07-NOV-2001) Department of Genetics, Washington
Submitted (07-NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jun 7, 2001 this sequence version replaced gi:13677176.
On Jun 7, 2001 this sequence resion replaced gi:13677176.
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MO 63108, USA
5 (bases 1 to
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-156B7; the clone sequenced to the right is RP11-536I18, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-575C6; actual end is at base position 180956 of RP11-575C6.
                                                                                                                                                 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://acapac.med.buffalo.edu)
VECTOR: pBACe3.6

INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence form more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-JUL-2001) Genome University School of Medicine, MO 63108, USA
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Submitted (20-APR-2001) Genome
University School of Medicine,
                     The sequence from base position 134614 to PCR product of RP11-575C6 BAC DNA.
                                                                                                                                                                                                                                                                                                                            SOURCE INFORMATION:
The RPCI-11 human E
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu/gsc
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   Location/Qualifiers
                                     /note="similar 1 ue97c04.y1" 5169. .5675
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4712. .5400
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3971. .41
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330. .1055
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553. .620
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1128. / 77.
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1364. .2264
(NID:g11005902)
                   /note="similar
                                                                                                 5106
                                                                                                             /note="similar to (NID:g10949704)"
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1210. .1243
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(NID:g13456766)"
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Chemistry: Dye-primer ET; 48% of reads
Chemistry: Dye-terminator Big Dye; 44% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178616 bases at least Q40
Consensus quality: 178729 bases at least Q30
Consensus quality: 178811 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 1181802; sum-of-contigs
Quality coverage: 14.71 in Q20 bases; sum-of-contigs
                                          133
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Submitted (10-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Aug 9, 2001 this sequence version replaced gi:9958173.
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Waterston, R.H.
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                       GGGTGAGTGCCTGTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTGTTTCT 192
                                                                                                                                                                   TATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGAGCA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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     GGGTGAGTGCCTGTTGCCAAGGTGGCCTCTTCAACAGGAAAACCACAATATTTTTGTTTCT 153159
                                                                         CGTGGAGTTAGGCAGGTTAGGGGACTCGGAGGACTGCGATGGTGCCAGGAAAGGGTGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-155P18"
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Homo sapiens BAC clone RP11-575C6
AC007256
AC007256.5 GI:14327871
                                                                              Direct Submission
Submitted (07-APR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                 4 (bases 1 to 181150) Waterston, R.H. Direct Submission
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Du, F., LaPlant, Y., Doe
                                                                       MO 63108,
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                                                                                                                                                                                 Unpublished
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99063792
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Sulston, J.E. and Waterston, R.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                               (bases
                                                                       USA
 (19-APR-2001) Genome
                                                                                                                                                               1 to 181150)
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                   Doebber, A.
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                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae;
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Sequencing
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complete sequence

PRI 07-NOV-2001

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671 153574 611 491

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Euteleostomi;

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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    Pred.
    No.
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1: gb_ba:*
2: gb_htg:*
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5: gb_pat
7: gb_pat
7: gb_pl:
9: gb_pr:
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Gapop 10.0 , Gapext 1.0
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the number of results predicted by chance to have a
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gb_htg:*
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gb_ph:*
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em_htgo_mus: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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L513346 Mouse D	.C095247 Rattus n	.P005545 Oryza sa	107270 Rattu	113915 Rattus no	AL401455 T3 end	110354 Rattus	C095069 Rattus no	AC069018 Mus mi	110338 Rattus n	ontinuation (2 o	C114068 Rattu	C097904 Rattus n	.C084799 Mus musc	101859 Mus musc	C103270 Rattus n	.C103270 Rattus n	.C083762 ното sap	429315 Homo sa	11282	107184 Rattus	112440 Rattus	103197 Rattus	091553 Trypand	110348 Rattus n	007524 Homo sa	6132 Human DN	117170 Rattus n	099291 Rattus	L390844 Human	064809 Homo	ontinuation (5	C116367 Orvza	C110348 Rattus	380342 Homo san	6494 Segmence	ACCOCC HOMO SEE	98172 H saniens	134419 Sequenc	R211527 Sequence	AFA22925 Homo sapt	des cuoti record	38981 HOMO Sap	007356 Homo sab	074016 Homo can	scription

## ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AC074016
Waterston, R.H. The sequence of Homo sapiens clone	<pre>ELNKATYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 179216)</pre>	Homo sapiens	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.	AC074016.5 GI:15144340	SEQUENCE, 2 unordered pieces. AC074016	RP11-155P18, WORKING	AC074016 179216 bp DNA linear HTG 09-AUG-2001	

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Sequence 3525, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Marien, Negappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3525
LENGTH: 434
TYPE: DNA
ORGANIEM: Bos taurus
OTHER INFORMATION: Clone ID: 16-BOVMS1-023-Q1-E1-D11
US-09-960-352-3525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-04-07
2000-05-30
2000-05-30
2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 166
SEQ ID NO 166
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OPHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (5950, 5973, 8958)
US-10-239-676-166
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US-09-960-352-3525/c
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Search completed: July 10, 2003, 22:35:45 Job time : 162 secs
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                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.8%; Score 32; DB 9; Length 13606; Best Local Similarity 48.4%; Pred. No. 27; Matches 89; Conservative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12230 AAAT 12233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12110 ATTTGTTTTAGGGATTTTTTGTTTTTTTGGTTATAGTTTTTGGGTTTTAGGAAGGTGGA 12169
                                                                                             366 GGGGGGCCTTTAGTTTGGGGAGGCAAAGGGATTTTCCCGTTGGTTTGGGGGGTACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             597 AGIGTITICACAGGTICICCITCTITIATCTTITIGTGTITITITICGAGCCATGGGGGTI 656
                                                                                                                                                                                                                                            543 GGTGAAGTTTTCTCTCTCTCGGAGACCAGATTCTGCCTTTACGCTGGAGGGAAGTGTT 602
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                                                                                                                                                                                                                                                                                          ch 4.7%; Score 31.8; DB 10; Length 434; Similarity 57.6%; Pred. No. 4.8; 57; Conservative 0; Mismatches 42; Indels 0
                                                                                                                                                                                                                                                                                             0;
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FEATURE:
NAME/KEY: unsure
LOCATION: (4779)
US-10-172-086-35
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US-10-172-086-35
(Sequence 35, Application US/10172086
Publication No. US20030113750A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
APPLICANT: Epigenomics AG
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                               δÃ
                                                    Query Match
Best Local Similarity
Thes 91; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-764-891-8090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-764-891-8090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10.31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8090
LENGTH: 6093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8090, Application US/09764891 Publication No. US20030077808A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 116
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.8%;
Best Local Similarity 56.0%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Method and nucleic acids TITLE OF INVENTION: of prostate tumors
                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE
                                                                                                                                                                                                     FEATURE: CTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                 ENGTH: 6271
1023
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                               TGGAGGTGTGTTTGCACGTCAGAGCCTGCATTTATGTAATATAGTTT 140
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                                                                        Conservative
                                                                                     4.8%;
48.1%;
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Pred. No. 15;
0; Mismatches
                                                                                     Score 32.2;
Pred. No. 15;
                                                                    Mismatches
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                                                                                                    Length 6271;
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                                                                  Indels
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                                                                 Gaps
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RESULT 14
US-10-239-676-166
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-572-11
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US-10-161-572-11
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CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR PPLICATION NUMBER: US 60/328,605
PRIOR PRILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10035E29.7
DE 10043826.1
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/10161572 Publication No. US20030087266A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Publication No. US20
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                      Sequence 166,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                  APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-097C-PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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Local Similarity 63.6%;
2S 49; Conservat:...
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                                                                                                                                                                                                                                                                                                                               Application US/10239676
o. US20030082609A1
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Pred. No. 76;
0; Mismatches
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; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Human
US-08-755-235-3
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; LOCATION: (15565, 15570, 15574, 15580, 15585..15586, 15589..15590, 17255)
US-10-239-676-53
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US-08-905-709-3/c
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APPLICANT: Schmidt, Ann Marie
APPLICANT: Win Jun
TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
FILE REFERENCE: 0575/50159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/755,235
CURRENT FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Stern, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                  APPLICANT: Stern, David
APPLICANT: Schmidt, Ann M.
TITLE OF INVENTION: A METHOD TO PREVENT ACCELERATED
TITLE OF INVENTION: ATHEROSCLEROSIS USING (SRAGE) SC
TITLE OF INVENTION: ADVANCED GLYCATION ENDPRODUCTS
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                  ZIP:
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                  COUNTRY:
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es 48; Conserv
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1185 Avenue of the Americas
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PC-DOS/MS-DOS
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Pred. No. 20;
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SEQ ID NO 512
LENGTH: 1426
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/195,604 PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CLASSIFICATION: 514
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                             541 GTGGTGAAGTTTTCTCTTTCTCTCGGAGACCAGATTCTGCCTTTACGCTGGAGGGAAGTG 600
                                                                                               481 TGTTCGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTACCCCTGCAGTTCCTTCT 540
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48; Conserv
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GTTGTTTTTATTTACATTTGTCACGTTGTTGTAAGAGAATGTTAACATGGTATAAAAACTC
                                                                TGGCAGAATGATTATTCTGTACCCTGGTTGATGTGTAGAGTAGATTGTCTGGTGCTCTCA
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Howes, Steven H.
Resnick, Richard J.
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Clark, Hilary
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Pred. No. 5.8;
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Pred. No. 6.8;
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US-09-948-783-103; Sequence 103; A
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SEQ ID NO 103
LENGTH: 704
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FILE REFERENCE: P02028H
CURRENT APPLICATION NUMBER: US/09/892,877
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 461
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PRIOR APPLICATION NUMBER: 09/437,658
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/948,783
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,846
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LOCATION: (287)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                               OR APPLICATION NUMBER: 60/085,093
OR FILING DATE: 1998-05-12
OR APPLICATION NUMBER: 60/085,094
OR FILING DATE: 1998-05-12
OR APPLICATION NUMBER: 60/085,105
OR FILING DATE: 1998-05-12
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Local Similarity 52.6%;
nes 71; Conservative
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                                    APPLICATION NUMBER: 60/085,922 FILING DATE: 1998-05-18 APPLICATION NUMBER: 60/085,921
                                                                                             APPLICATION NUMBER: 60/085,924 FILING DATE: 1998-05-18
                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                          APPLICATION NUMBER: 60/085,180 FILING DATE: 1998-05-12 APPLICATION NUMBER: 60/085,927
FILING DATE: 1998-05-18
APPLICATION NUMBER: 60/085,923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09948783
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                                                                                                                                                                        1998-05-18
                                                                                                                                                                                                                                                                                                                                                                 1999-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted proteins
                                                                                                                                                                                        60/085,927
                                                                                                                                                      60/085,906
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Pred. No. 3.4;
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RESULT 7
US-10-239-676-53
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; LOCATION: (287)
; OTHER INFORMATION: n
US-09-948-783-103
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PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 465
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 103
                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2
2000-04-06
2000-04-07
2000-06-30
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SEQ ID NO 53
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Best Local :
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DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,928
PRIOR FILING DATE: 1998-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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TYPE: DNA
                                                                                   FEATURE
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                                       FEATURE:
                                                                        NAME/KEY: unsure
                                                                                                      NAME/KEY: unsure
LOCATION: (515, 1325,
                                                                                                                                           OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                LENGTH: 17421
TYPE: DNA
 NAME/KEY: unsure LOCATION: (9222,
                                                      OCATION: (7028,
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9233, 9261, 12655, 12689, 12792, 13398, 14469, 15562..15563;
                                                      7082, 7179,
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                                                      8249, 8252, 8254, 8269, 8275, 8278..8279;
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Pred. No. 3.
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                                                                                                          3707, 5320,
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RESULT 3
US-09-918-995-12139/c
US-09-918-995-12139/, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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US-10-239-676-8
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SENERAL LIFTONE....

APPLICANT: HYSEQ, Inc.
APPLICANT: HYSEQ, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQ:
TITLE OF INVENTION: FROM VARIOUS CDNA LIB
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
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Best Local Similarity
Matches 94; Conserv
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LENGTH: 7148
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Publication No. US20030082609A1
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DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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2000-04-06
2000-04-07
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CURRENT FILING DATE: 2002-09-24
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TITLE OF INVENTION: Diagnosis of Diseases Associated with
FILE REFERENCE: 5013.1003
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ORGANISM: Artificial
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PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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48.5%;
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                                                                          CDNA LIBRARIES
                                                                                          ACID SEQUENCES OBTAINED
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RESULT 5
US-09-892-877-103
Sequence 103, Applicat
Publication No. US2003
GENERAL INFORMATION:
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US-09-764-891-6031/c
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SEQ ID NO 6031
LENGTH: 7010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12139
LENGTH: 570
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Best Local :
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Best Local
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TITLE OF INVENTION: Nucleic Acids, Protei
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)...(570)
OTHER INFORMATION: n = A,T,C
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                                                                                                  2842 AGACGTGGTTAA 2831
                                                                                                                                                       2962 CTGACTTTCCTCCAAGATTGGCATGATATCTTTGAATTTGCTTCCAGATGCACACTTAAG
                                                                                                                                                                              527 CIGCAGTICCTICIGGIGAAGTITICICITICICICGGAGACCAGAITCIGCCTITAC
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Pred. No. 10;
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Pred. No. 2.6;
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Application US/09892877 o. US20030077809A1

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
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US-10-239-676-8
US-09-918-995-12139
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US-09-982-877-103
US-09-9848-783-133
US-10-239-676-53
US-08-9782-830A-512
US-09-822-830A-512
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US-10-172-086-35
US-10-172-086-35
US-10-161-572-11
US-10-239-676-136
US-10-198-846-1473
US-09-976-740-50
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Sequence 12, Appl Sequence 8, Appl Sequence 12139, Ap Sequence 103, App Sequence 103, App Sequence 3, Appl Sequence 3, Appl Sequence 31, Appl Sequence 35, Appl Sequence 35, Appl Sequence 11, Appl Sequence 16, App Sequence 50, Appl Sequence 50, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/003,132
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/249,004
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 2145
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-003-132-12/c
US-10-003-132-12/c
; Sequence 12, Application US/10003132
; Publication No. US20020192750A1
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                                                                                                                                                                                                                                                                                                                                      Query Match 5.2%; Score 34.6; DB 9; Length 2 Best Local Similarity 29.4%; Pred. No. 1.4; Matches 82; Conservative 48; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fox, Brian A. APPLICANT: Gao, Zeren APPLICANT: Shoemaker, K
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Shoemaker, Kimberly E.
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Minimum Maximum

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Sequence 109, App	equence 109, Ap	e 109, Ap	e 109, Ap	: 109, Ap	109, Ap	e 109, Ap	ce 109, Ap	109, Ap	се 109, Ар	109, Ap	e 109, Ap	ĄĘ	109, A	Ą	109, Ap	109, Ap	equence 109, Ap	e 109, Ap	eguence 17,	e 17,	equence 17,	equence 17,	equence 17,	equence 17,	Sequence 9891, Ap

TITLE OF INVENTION: NEUROPILIN HOMOLOG ZCUB5 FILE REFERENCE: 00-62

1721 GCRTCNGTNSWNACNCCNGCYTCYTCNGCRTCNGTRTCCATNGGNCKRAANGTNSWNCCY 1601 GTDATNARRTCNARYTTYTGNGTCATYTCYTTYTCRTTRTCRTANSWDA-TNGTRAAYTC 1543 463 TAAACAGGAAACATTTCTTGTTCGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTT 522 343 GAGTCAGTATAAATGCTTTCCAATAAAGCATGTCCAGCGCTCGGGGCTTTAGTTTGCACGT TINCKNGTNACNGTNCCNGTNCCDATCATNARNGGYTGYTGRTARTCNGCCATRTCNSWN 1. 1602 .462 1662 402

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US-09-360-220-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09360220 Patent No. 6046308 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
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                                                                                                                           TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2241 base pair
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: FOLEY, HC
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                                               FEATURE:
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                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                               NAME: Arnold, Beth E. REGISTRATION NUMBER: 35,430 REFERENCE/DOCKET NUMBER: MI
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
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                                                                                            STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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TVENTION: THERAPBUTIC COMPOSITIONS AND METHODS AND
TOWNS OF DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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55.6%;
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Pred. No. 3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                               Version
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                                                                                                               US-08-460-512-1
                                              Query Match
Best Local Sim
Matches 74;
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GENERAL INFORMATION:
APPLICANT: MEYERO
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Best Local
                                                                                                                                                                                                                TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1457 base pairs
TYPE: nucleic acid
STBANEGURES: (5:0-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
REGISTRATION NUMBER: 31,80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                            FEATURE:
                                                                                                                                                                           MOLECULE TYPE:
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APPLICATION NUMBER:
                                                                                                                           NAME/KEY:
LOCATION:
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER;
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                       STRANDEDNESS:
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79; Conserv
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TGAAATTTGAAGAACAGGGCCAAGGATGGGAACTCAGCCTGAGCACGGGTTGATCCGGAG 105
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                                               Conservative
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                                            Score 30.2; DI
Pred. No. 3.3;
0; Mismatches
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Pred. No. 3.6;
0; Mismatches
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RESULT 12
US-09-360-220-16/c
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Best Local :
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                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
                                                                                                                                                                                       APPLICANT: Glucksmann, M. Alexandra
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS AND
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING TRBP
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
                 CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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 APPLICATION NUMBER:
                                                                                                                       STATE: MA
COUNTRY: USA
ZIP: 02109-2170
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ZIP: 02109-2170
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nucleic acid
DEDNESS: single
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US/09/360,220
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Pred. No. 1.
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US-08-840-146-1/c
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Patent No. 6037173
GENERAL INFORMATION:
                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFMARE: PSTEM: PC-DOS/MS-DOS
SOFFMARE: PSTEM: PC-DOS/MS-DOS
SOFFMARE: PSTEM: PC-DOS/MS-DOS
SOFFMARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,146
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ATROLA, BETH E
REFERENCE/DOCKET NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-018.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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NAME: Arnold, Beth E.
NAME: Arnold, Beth E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Glucksmann, M. Alexandra
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS AND
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING TRBP
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CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                   TELECOMMUNICATION INFORMATION:
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STREET: C...
ATTY: BOSTON
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                                       TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-2170
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les 79; Conserv
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FILING DATE: 11-APR-1997
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55.6%;
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RESULT 9
US-08-633-148-1/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 957 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08633148
Patent No. 5864018
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                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR.1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MORSEK, PALIFICANT: MORSEK, PALIFICANT: NAGASHIMA, MARIKO
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
APPLICANT: HOLLANDER, DORIS A.
APPLICANT: THE ANTIBODIES TO ADVANCED GLYCOSYLATION
APPLICANT
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALLEGRNIA
                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ANTIBODIES TO ADVANCED GRAPHTIDES AND USES THEREFOR NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                ATTORNEY/AGENT INFORMATION:
NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
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                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MURPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 0146
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 45; Conserv
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CALIFORNIA
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ER: 014618-005600US
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014618-005600US
                                                                                                                                                     Version #1.30
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RESULT 11
US-08-840-146-16/c
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; LOCATION: (1049)...(2086)
US-09-457-066-42
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; MOLECULE TYPE:
US-08-633-148-1
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Sequence 16, Application US/08840146
Patent NO. 6037173
Patent INFORMATION:
APPLICANT: Glucksmann, M. Alexandra
APPLICANT: Glucksmann, M. Alexandra
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS AND
TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR DISEASES INVOLVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Glibertson, Debra G.
APPLICANT: West, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 42
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Best Local:
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Best Local Similarity
Matches 45; Conserv
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3571
TYPE: DNA
ORGANISM: Mus musculus
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                                                                                                                                                                                                                    608 AGGTTCTCCTCCTTTTATCTTTTGTGTTTT 637
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EDNESS: double
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58.9%;
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Pred. No. 3.
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                               Mismatches
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RESULT 7
US-08-463-772-32
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                                                               Sequence 32, Application US/08463772 Patent No. 6065501 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAX-1992
PRIOR APPLICATION DATE:
APPLICATION UNMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS. SOFTWARE: ASCII(text) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
              APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS
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STREET: ...
STREET: ...
AMY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Matthew P. Vincent REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 19-MAY CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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DEDNESS: double
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US-08-463-772-32
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US-08-633-148-3/c
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 Sequence 3, Application US/08633148 Patent No. 5864018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 77; Conserv
                                              APPLICANT: MORSER, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO
TITLE OF INVENTION: END-PRODUCT RI
NUMBER OF SEQUENCES: 23
                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEW P VINCENT
REGISTRATION NUMBER: 36,70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSENT & STREET: TWO EMBARCADERO CENTER, 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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STREET: 60
CITY: Bost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2022 base pairs TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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join(1137..1211, 1211..1678, 1680..1790)
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51.3%;
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 & CREW LLP
8TH FLOOR
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Best Local S
Matches 77
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                                                                                                                                                                                                                                                                                                                          TELEFAX: 616-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/888,178 FILING DATE: 26-MAY-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: D-Type Cyclin and Uses NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: CS:
                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 19930
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CITY: Lexington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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CCCAGGCTGGAGTGCAGTGGGCGCGATCTC 688
                          TTCCTTCTGTGGTGAAGTTTTCTCTTTCTC 562
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                                                                                                                                                                  Score 33.2; DB Pred. No. 0.36; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reynolds, P.C
                                                                                                                                                                                              DB 5;
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; LOCATION:
US-08-464-517-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MII-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/
FILING DATE: 26-May-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 16-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: FEATURE:
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MEDIUM TYPE: F1
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
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659
                               533 TTCCTTCTGTGGTGAAGTTTTCTCTTTCTC 562
                                                                                                                                       539 TCTCCTGCCTCAGACTCCTGAATAGCTGAAATTACAGGCACCTGCCACTACGCCTGGCAA
                                                                                                                                                                         413 TCTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAACAGGAA 472
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CCCAGGCTGGAGTGCAGTGGGCGCGATCTC 688
                                                                     ATATTTTTTGTTTGTTTGTTTGTTTGTTTTGTTTTGAGACAGAGTCTCTCTGTCG
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                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           double
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51.3%;
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RESULT 6 US-08-246-361A-32

Sequence 32, Application Patent No. 5998582

US/08246361A

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GENERAL INFORMATION:

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                                                            Query Match
Best Local S
Matches 74
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Best Local 9
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          FILING DATE: 16-APR-1996
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER: IL 116,588
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APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
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LENGTH: 2887 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: IL 114,986 FILING DATE: 17-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: IL 1: FILING DATE: 16-JUL-1995
                                                                                                                                                                                                                                           APPLICATION NUMBER: IL 117,932 FILING DATE: 16-APR-1996
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: IL 11 FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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TOPOLOGY: lin
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                    573 GATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGT
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                                                                          Similarity
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Pred. No. 3.
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; CLONE: pTZgpt-F1s
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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LENGTH: 7218 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/935,313
FILING DATE: APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT FOWLFOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1000
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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ZIP: 22313-0299
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25; Conserv
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            nucleic search, using sw model
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
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PCT-US96-10521-14
US-08-232-463-14
US-08-2463-17-32
US-08-464-361A-32
US-08-463-772-32
US-08-633-148-3
US-08-633-148-3
US-08-633-148-1
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US-09-221-0178-478
US-09-221-0178-478
US-08-232-463-14
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e L	Sequence 1, Appli	Sequence 2, Appli	Sequence 6, Appli	2	Sequence 52, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Patent No. 5455158	Sequence 16, Appl	Sequence 16, Appl	დ დ	Sequence 7, Appli

## ALIGNMENTS

; REGISTRATION NUMBER: 25,618 ; REFERENCE/DOCKET NUMBER: WALLACH=19 ; TELECOMMUNICATION INFORMATION:	Y/AGENT INFORMATION: Browdy, Roger L.	; APPLICATION NUMBER: IL 117,932 ; FILING DATE: 16-APR-1996	TION DATA:	APPLICATION NUMBER: IL	99	LICATION NUMBER: IL	0	ATION NU	TION DATA:	: PITTING DATE: 16-IIII1005	OR APPLICATION DATA:	ING DATE: 14-JUN-1996	APPLICATION NUMBER:	; FILING DATE: 16-JAN-1998	; APPLICATION NUMBER: US/08/983,502	PatentIn	COMPOTER: IBM PC COMPACIBLE	; MEDIUM TYPE: Floppy disk	BLE FORM:	0	OUNTRY:	STATE: D.C.	TTY: Washington	: STREET: 419 Seventh Street N.W. Ste 200	CE ADDRESS:	R OF SEQUENCES: 34	OF INVENTION: AND OTHER PROTEINS	NVENTION: MODIFIED OF THE TINOTION OF TAC	,	Mark P. B	APPLICANT: David	399327	983-502	RESULT 1
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RESULT 15
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Best Local Similarity 43.5%;
Matches 87; Conservative 1
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                       622 TTATCTTTTGTGTTTTTTTT 641
                                                                                   525 CCAGGAGTCTCKGTTCNNKTNTNNTGGAGNCCNTGTTGGKGTTNTTTGGTTTAKTTTGTT
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                                                                                                                                                                                                                                                                                                       465
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Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr -

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -

collaboration with the European Drosophila melanogaster BAC on trp://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.

Drosophila melanogaster

Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Bubtera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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(bases 1 to 805)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila m
/db_xef="taxon:7227"
/clone="BAQNO6044"
/clone_1ib="DrosBAC"
/plasmid="pBeloBAC11"
/plasmid="pBeloBAC11"
/note="end : Sp6"
a 136 c 105 g 1
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Pred. No. 29;
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Search completed: July 10, 2003, 21:27:45 Job time: 1353 secs

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Matches 97; Conserv
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83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-85-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1080 bp DNA linear GSS 01-NOV-200
Pan troglodytes DNA, clone: PTB-022A16.R, genomic survey sequence.
AG043660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC Library clone:PTB-022A16.R.
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GSS.
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R.Site 1
R.Site 2
                                     Conservative
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                                                                                                                  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
55 c 287 g 67 t
                                                                                                                                                                                         /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-022A16.R"
                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                     49.4%;
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                                                     Score 38.6;
Pred. No. 2
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                                   85;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library or filters for hybridization from the BACRAC Resource Center can be found at http://bacnac.med.buffalo.edu/Afrosophila bac ben
                                              485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749
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AL068307
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97; Conserv
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone_lib="RPCI-98"
/note="end : T7"
a 148 c 112 g
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/db_xref="taxon:7227"
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35.0%;
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; Pred. No. 26;
42; Mismatches
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source
                                                                                                                                     Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library or filters for hybridization from the BAC clones, the entire library or filters for hybridization from the BACAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR37D10"
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                                                                                                                                                                                                                                                                                Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or 1
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Other_GSSs: RPCI-11-360P2.TJ
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
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GSS.
                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
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           /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
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/note="end : T7"
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/clone="RPCI-11-360P2"
/clone_lib="RPCI-11"
                                                                                     /sex="Male"
                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:7638217"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 784)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                           BI857533.1
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Direct Submission
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/db_xref="taxon:7227"
/clone="Back20D15"
/clone_lib="RPCI-98"
/note="end: TET3"
80 c 89 g 437 t 102
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Pred. No. 5.
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segref@genoscope.cns.fr
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E:5393212 5',
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1 Similarity
47; Conser
                                                                                                                                                                                         High quality sequence stops: 293 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 797 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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T86125
                                                                                                                   High quality sequence stop: 293
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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Plate: LLAM12002 row: c column: 05
                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 797
                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
1 (bases 1 to 398)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE: 114897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGCGTCCGCCAGATTCTGCCTTTCTGCTGGAGGGAAGTGTTTTCACAGATTATATTC
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/lab_host="DHIOB (phage_resistant)"
/note="Organ: breast; Vector: pcW-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHM_MGC Library."
a 157 c 194 g 183 t
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/db_xref="taxon:9606"
/clone="IMAGE:5393212"
/clone_lib="NIH_MGC_87"
                       /organism="Homo sapiens"
/db_xref="GDB:470514"
/db_xref="taxon:9606"
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/clone="IMAGE:114897"
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Soares fetal liver spleen INFLS Homo sapiens cDNA clone
97 3' similar to contains Alu repetitive element;, mRNA
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79.7%;
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Pred. No. 13;
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AL298521
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122009 of
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57; Conserv
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BQ941968
Tetraodon nigroviridis
Tetraodon nigroviridis
                            GSS; genome survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ941968 940 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8835770 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6421760
                                                 AL298521.1 GI:8037101
                                                                                                                                  CNS04NC0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, N
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                     TCTTTCTCTCGGAGACCAGATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCT
                                                                                                                                                                                                                    ATTC 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                      281
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                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/clone=lib="NH_MGC_18"
/clone_lib="NH_MGC_18"
/clone_lib="NH_MGC_18"
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/tissue_type="large cell carcinoma"
/lab_host="PH108 (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: xhoI; Site_2:
ECGRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a 200 c 236 g 223 t
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Query Match
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                                                                                                                                                                                    792 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR20D15 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL053997
Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 792)
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GSS.
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Submitted (12-APR-2000)
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Roest-Crollius, H., Jaillon, O.,
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Roest-Crollius, H., Jaillon,O., Dasi
Bernot,A., Fizames,C., Wincker,P.,
Saurin,W. and Weissenbach,J.
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Quetier,F., Saurin,W., Bernot,
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 804)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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603035156F1 NIH_MGC_115
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Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                           TTGTTCAAGCCCTG 136
                                                                                                                                                            CTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTTGTGTTT 636
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                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: pooled brain, lung, testis; Vector: pcMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNI source annonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library 1s oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5176548"
/clone_lib="NIH_MGC_115"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), gen
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN17J04 of DrosBAC library from Drosophila melanogaster (fruit
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Drosophila melanogaster
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1 (bases 1 to 1101)
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                                                                                                                TKBBKKTTKKKTKTTKTKKSGKKBKKKKKSTSBKYBVGYBBYGCGCTSBSSCTKTCYYBC
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/db_xref="taxon:7227"
/clone="BACN17J04"
/clone_lib="DrosBAC"
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/note="end : SP6"
126 c 100 g
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                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genme Analysis, German Cancer
Clone from S. Wiemann, Molecular Genmen Research Center (DKT2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiemann,S.)
Unpublished (1999)
Contact: Bloecker H
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421 bp mRNA linear EST 22-MAR-DKFZp686E18155_rl 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686E18155 5', mRNA sequence.
                                                                                                                                                                                            This clone (DKP2p686218155) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloecker, H., Boecher, M., Brandt, P.,
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1 (bases 1 to 421)
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nilarity 96.2%;
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 95
/clone="DKFZp686E18155"
/clone_1ib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplEx2; Site_1: Sfil
cDNA-collection"
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/clone_lib="313 (synonym:
/dev_stage="adult"
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dKfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wiemann, S.)
Unpublished (1999)
Contact: Bloecker
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DKFZp686M12156 5',
                                                                                                                                                                                                                                                                                                                        No s1 sequence available.
This clone (DKF2p666M12156) is available at the R2PD ir Please contact the R2PD: Ressourcenzentrum, Heubherweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de...
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Mammalia; Eutheria; Primates;
1 (bases 1 to 463)
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                               GAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGT
GAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGT
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                                                                                                                               cDNA-collection"
98 c 110.
                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="DKFZp686M12156"
/clone_lib="686 (synonym: hlcc3)"
                                                                                                                                                                                                 /tissue_type="human skeletal
/dev_stage="adult"
                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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Catarrhini; Hominidae
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RESULT 1
AL600571
LOCUS
DEFINITION REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE COMMENT ORGANISM JOURNAL Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 522)

1 (bases 1 to 522)

Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.

EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)

Unpublished (199)

Contact: Ansorge W AL600571

522 bp mRNA linear EST 14-AUG-2001

DKFZp313F1234\_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone

DKFZp313F1234 5', mRNA sequence. EST AL600571 AL600571.1 GI:15164077 namur

ALIGNMENTS

Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone Insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.

No s1 sequence available. This clone (DKFZp313F1Z34) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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1	Db Qy	Ф	дь Ф	Оу	Qy
	594 5595	534 5655	474 5715	414 5775	354 5835
	594 GGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGTGTTTTTTTT	534 TCCTTCTGTGGTGAAGTTTTCTCTTTTCTCTCGGAGACCAGATTCTGCCTTTACGCTGGAG 593  :  :  :  :  :  :  :  :  :  :	474 CATTICTIGITGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTACCCTGCAGT 533 5715 RCYRARCYSCYTCYTYSYDASTCYTSRGTBCYTTBYSTBIBNCRCNCYSDSTYRANCYSS 5656	414 CTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAACAGGAAA 473 :::      :: :  :  :  :  :  :  :  :  :  :	354 AATGCTTTCCAATAAAGCATGTCCAGCGCTCGGGCTTTAGTTTGCACGTCCATGAATTGT 413 : ::::   ::    ::  ::::  :::   :: 835 DAYSDYDASTSDTTSRSDSTTTCYTSTNSTSRDNSTRCTTRCYSSRCYTYSYSTCYTSDY 5776

Search completed: July 10, 2003, 21:31:37 Job time: 225 secs

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17-NOV-2000;
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17-NOV-2000
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, and polynucleotides may be used to prevent.
                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and merastasis.
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2000US-0251988.
2000US-0256719.
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK5490 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cellulose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene encoding a subunit of cellulose synthase
                                                                                                                                                                                                         A gene encoding a cellulose synthetic equipment - in the amount of cellulose synthesised in a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vigna angularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA10595
  Sequence
                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                         (MIZU/) MIZUNO K.
(OJIP ) OJI PAPER CO
                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP2000060568-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA10595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 256 BP; 82 A; 35 C; 49 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                   2000-342371/30
)B; AAY85180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 AAGCCAAGTACGAATGAACCAGACCACTTCCTCCTTTTTTTCTGAACGATCTACCCGCAT 172
                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAAGAA
  6741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAGTGCTGAGGTTTGATCAAGGCAAAGGGAAACTTCCTATTCCCAGACCCTTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGGCATGGTGGCTCACTCCTGTAACCCCAAACTGTGGGAGGCTGAGGCTGGTGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 22-31; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGAGTCCAGGAGTTTGAGACCAGCCTGAGCAACATGGTGAAACCCTGTTTCTATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                    98JP-0239998
                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0239998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299
  1712 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellulose production; increase yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6741
  870
                                                                                                                                                                       Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB:
Pred. No. 1.4;
0; Mismatches
  C; 1468
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  <u>و</u>
  1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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  Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
  1317
                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                             the
  other,
                                                                                                                                                                                                                             improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
                                                                                              of of
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Query Match Best Local S Matches 59

Similarity

5.2%; 20.5%;

Score 35; Pred. No.

DB 21; 6.2;

Length 6741;

Mismatches

Indels

0

Gaps

0

Conservative

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RESULT 14
AAK81668
ID AAK81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 85
 31 JAN - 2000;
04 - FEB - 2000;
24 - FEB - 2000;
02 - MAR - 2000;
10 - MAR - 2000;
17 - MAR - 2000;
17 - MAR - 2000;
18 - APR - 2000;
07 - JUN - 2000;
28 - JUN - 2000;
07 - JUL - 2000;
11 - JUL - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune; haematopoietic; immune/haematopoietic
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New D-type mammalian cyclin - replaces for cell start in budding yeast and is hybridisation in biological samples to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-405720/50
P-PSDB; AAR44806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK81668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK81668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2020 BP; 553 A; 485 C; 463 G; 519 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beach DH
                                                                                                                                                                                                                                                                                                               17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                   WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITO-) MITOTIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    539 TOTOCTGCCTCAGACTCCTGAATAGCTGAAATTACAGGCACCTGCCACTACGCCTGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 TCTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAACAGGAA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 ACATTTCTTGTTCGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTACCCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 50.6
85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCTTCTGTGGTGAAGTTTTCTCTCTCTCGGAGACCAGATTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCAGGCTGGAGTGCAGTGGGCGCGTCTCAGCTCACTGCAAACTCTGC
 2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-01846350.
2000US-019874.
2000US-019874.
2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0214886.
2000US-0216480.
2000US-0216880.
2000US-0216880.
2000US-0217487.
2000US-0217487.
2000US-0217487.
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                                                                                                                                                                                                                                                                                                             2001WO-US01354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.2; DI
Pred. No. 3.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLN-type protein needed detected by antibodies of determine abnormal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D3 pseudogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 2020;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:36480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532
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   מיסים ליסים ליסים
26-JUL-2000
14-AUG-2000
11-AUG-2000
11-AUG
2000US-0240960
2000US-0241221
2000US-0241785
2000US-0241786
2000US-0241786
2000US-0241808
2000US-0241809
2000US-0241809
2000US-0241876
2000US-0244617
2000US-0244617
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2000US-0236369
2000US-0236302
2000US-02336802
2000US-0237037
2000US-0237038
2000US-0237038
2000US-0237040
2000US-0237040
2000US-0237040
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2000US-0235484.
2000US-0235834.
2000US-0235836.
2000US-0235836.
2000US-0236327.
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2000US-0232080
2000US-0232081
2000US-0231968
2000US-0231968
2000US-02323397
2000US-0232398
2000US-0232399
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2000US-0229513.
2000US-0230437.
2000US-0231438.
2000US-0231242.
2000US-0231243.
2000US-0231243.
2000US-0231244.
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2000US-0229287.
2000US-0229343.
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2000US-0225457
2000US-0225757
2000US-0225759
2000US-0225759
2000US-02256279
2000US-0225628
2000US-0225668
2000US-0227668
2000US-0227069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0234223.
2000US-0234274.
2000US-0234997.
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2000US-0232401.
2000US-0233063.
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2000US-0220964
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2000US-0233065
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RESULT 12
AAF98635/c
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     ID XXX ACC XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 81
03-SEP-1999; 99US-0152547.
16-MAR-2000; 2000US-0190347.
21-MAR-2000; 2000US-0191321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                             Human ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                              01-SEP-2000; 2000WO-US24199
                                                                                                                                                                                                                             WO200118542-A2
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF98635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF98635 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2819 BP; 787 A; 651 C; 571 G; 809 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 4923-4924; 11750pp; English.
                                                                                                                                                                    15-MAR-2001
                                                                                                                                                                                                                                                                                                                                            tumour; kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient;
(I) is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (\mbox{\bf d}) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2000; 2000US-255281P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasted in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGTTCTGCTTTCGTTGTCGTTTGTCTCGTCTATTCCTTGTGATTTTCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGTTCTGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGTGAAGTTTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCATCATTCCTGTGTTTCTGCCCGCCTCCGCCGGCG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful as a pharmacodyanamic or pharmacogenomic
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                                                                                                                                                                                                                                                                                                                                                                                                                    cancer cell expressed sequence
                                                                                                                                                                                                                                                                                                                                                                    cancer; identification; detection; characterisation;
                                                                                                                                                                                                                                                                                                                                            marker;
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RESULT 13
AAQ53209
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see AF98594 to AF98593 in a patient sample; and (2) the sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (1) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to AAF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention.
                                                                                                                                                            Homo
                                                                                                                                                                                     D-type; mammalian;
yeast; complement;
                                                                                                                                                                                                                                                                                                                AAQ53209 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 991; 1198pp; English.
                        25-MAY-1993;
                                                  09-DEC-1993
                                                                            WO9324514-A
                                                                                                                                                                                                                               Human cyclin
                                                                                                                                                                                                                                                          22-JUN-1994
                                                                                                                                                                                                                                                                                      AAQ53209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection, assessment, prevention and therapy comprises detecting changes in the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-211428/21.
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20-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 GGGAGGAGAGGGCTGGTCTGTGACTTCAGTGCTGAGGTTTGATCAAGGCAAAGGGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thompsho P,
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                                                                                                                                                                                                                                                                                                                                                                                 GTATCACT 172
                                                                                                                                                                                                                                                                                                                                                                                                             TTATTACT 337
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2000US-0220467
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                        93WO-US05000
                                                                                                                                                                                                                               pseudogene
                                                                                                                    Location/Qualifiers 1136..1793
                                                                                                       /*tag=
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54.78;
                                                                                                                                                                                        CLN protein; protein deficiency; cell cycle start; ds.
                                                                                                                                                                                                                                                                                                                DNA;
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                                                                                                                                                                                                                                                                                                                2020
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                                                                                                                                                                                                                                                                                                                ВP
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Pred. No. 1.
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26-MAY-1992;

92US-0888178

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RESULT 10
AAS46557
ID AAS46557
ID AAS46557
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AC AAS46
XX
AC AAS46
XX
DT 18-DE
XX
Human
KW Canc
KW Cyto
OS Homc
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PN W02(
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PN 015-
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Best Local
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor gene;
cancer; tumour; CpG dinucleotic
                          Claim 1;
                                                                                            Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS46557 standard;
                                                                                                                                                                                                                                                                                                   (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                   2001-602752/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          suppressor
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D5; Conservative
                                                                                                                                                                                                                                                                                                   EPIGENOMICS
                          SEQ
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; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
                          ID No
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                             279;
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Pred. No. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 105
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form of the printed specification, but was obtained in ele format directly from WIPO at
                                                                                                                 17-FEB-2000; 2000US-183319P
                                                                                                                                                                             20-FEB-2001; 2001WO-US05171.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer;
pharmacogenomic marker;
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47.79;
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Pred. No.
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ARESULT 8
ABQ49947/c
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-Cp6-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The meth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate temethod for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                          Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-2000;
05-SEP-2000;
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SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
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2000DE-1044543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
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                                                                                                                                                                                                                                                                           Sequence Listing; 56pp;
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                                                                                                                                                                                                                 New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining status, e.g. in diagnosis or treatment of cancer -
                      The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis associated genes (i having sequences (ABO66971-ABO67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or
                                                                                                                                                                                                              status, e.g.
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single-nucleotide

polymorphisms,

in angiogenesis-related

(II)

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CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression level in an unactivated CC (GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent Capable of modulating (M2) GA by contacting GC with an agent Capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC evel of expression in a sample of the tissue of gene(s) from GS, where CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression of the gene is indicative of inflammation; where CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or constanting a tissue having CC inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting a tissue having CC inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for adetecting GCA; M2 is useful for CC detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, cc and allergic response in a subject was agent capable of modulating GCA preferably in a niflammation, thrombosis, cardiac reperfusion injury, renal conflammatory bowel disease, Crohn's disease, ulcerative colitis, conflammation, protozoal infection, fundal infection, with infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 1294; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beazer-Barclay Y,
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rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA differentially expressed in granulocytic cells #1294.
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                                           parasitic infection,
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                tic infection, protozoal infection, fungal infection and for treating one of the above conditions. The present
  represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            granulocytic cell; DNA chip; bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parasitic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sterile inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weissman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      injury; renal reperfusion injury; ARDS;
a gene differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protozoal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma;
                                       infection and M5
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RESULT 7
ABQ49946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpC-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cycosine (C) but not methylated C, to uracil. then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders cof the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                             Claim 12;
                                                                                                                                                                                                                                                                                       Determining the degree of cytosine methylation in for diagnosis and prognosis, comprises selective hamplicons from chemically treated DNA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-2000; 2000DE-1043826
05-SEP-2000; 2000DE-1044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2001; 2001WO-EP10074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200218632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ49946 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2887 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 GATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GTTTTTTTCAAGCCCTG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTTTTTCGAGCCATG 650
                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                          56pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                            Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             853 A; 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
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                                                                                                                                                                                                                                                                                                                                                                                      Berlin
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                                                                                                                                                                                                                                                                                                                                                                                      ζ×,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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No. 2.
                                                                                                                                                                                                                                                            56pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 T; 0 other;
                                                                                                                                                                                                                                                          German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                       ı genomic DNA,
hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2887;
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                                    respiratory
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                                                                                                                                                                                                                                                                                                         useful
of
                                                                                   The method
                                                  disorders
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RESULT 5
AAD03915
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                                                                                                                                                                                                                                                                       AAT61396, and AAT61405-T61411 represent coding sequences for different CC isoforms of MACH. MACH is a binding protein for the mediator of receptor CC toxicity (MORT-1) protein. MORT-1 binds to the FAS ligand receptor CC (FAS-R) death domain region, and triggers part of the cell death CC signalling cascade in mammalian cells. Vectors containing these CC sequences, the encoded proteins, and antibodies (Ab) against them are CC used to modulate the effect of FAS-R ligand or TNF on cells that carry CC FAS-R or p55-R. This is specifically for treating tumours, HTV-infected CC cells or other diseased cells, by control of apoptosis/programmed cell CC death. The encoded proteins are mediators of the cell death pathway CC initiated by TNF and FAS-R binding, i.e. it mimics or enhances the CC effect of MORT-1, e.g. in cases of septic shock, graft rejection and CC acute hepatitis, sequences encoding antisense molecules or ribozymes, or CC ab against the protein, are used. Compounds that inhibit MACH are CC potentially useful for controlling MACH activity e.g. in cases of CC autoimune disease, oligodendrocyte death in multiple sclerosis or CC AIDS-inhibited T-cell suicide. The MACH proteins can also be used to CC isolate and characterise other proteins and receptors involved in CC signalling and for ab production. The Ab can be used to purify the new CC proteins and for diagnosis of conditions involving abnormal function of CC FAS-R mediated cellular effects.
                                                                                                                                                                                                      Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1996;
16-JUL-1995;
17-AUG-1995;
14-SEP-1995;
02-JUL-2001
                      AAD03915;
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                                               AAD03915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 116-117; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New
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                                                                                                                                                                                                                                                      Sequence 2887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WEIN/)
                                                                                                                                                                                                       Local Similarity
nes 74; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w DNA encoding MACH protein that interacts with MORT-1 protein mediate intracellular effects of FAS or TNF receptors, partic. r regulating apoptosis in tumours, virus-infected cells etc.
                                                                                                                                 633
                                                                                                                                                                                573
                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEINWURZEL H.
YEDA RES & DEV CO LTD
                                                standard;
                                                                                                          GTTTTTTTCAAGCCCTG 78
                                                                                                                                GTTTTTTTTCGAGCCATG
                                                                                                                                                       GATTCTGCCTTTCTGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGT
                                                                                                                                                                               GATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGT
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                                                                                                                                                                                                       Conservative
(first entry)
                                                                                                                                                                                                                                                     BP;
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95IL-0114615.
95IL-0114986.
95IL-0115319.
95IL-0116588.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= MORT-1 binding protein (MACH) isoform alphal
                                                                                                                                                                                                                                                     853 A; 595
                                               DNA;
                                                                                                                                                                                                                10.7%;
                                               2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goncharov
                                                                                                                                 650
                                                                                                                                                                                                       0
                                                                                                                                                                                                      Score 71.6; DB 18; Pred. No. 2.2e-11; D; Mismatches 4;
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                                               ВP
                                                                                                                                                                                                                                                     625 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wallach
                                                                                                                                                                                                                                                     814 T;
                                                                                                                                                                                                                                                     0 other;
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                                                                                                                                                                                                                             Length
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RESULT
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632 60

DY X C X U

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The present sequence is a DNA encoding human Caspase-8 also known as CC MACH, FILCE and Mch5. Caspases are a family of cysteine proteases, that CC participate in the initiation and execution of apoptosis. Caspases exist CC as pro-enzymes, activated by cleavage into a large and small subunit. CC occurring after specific aspartic acid residues within the pro-enzyme sequence. The present invention relates to a method for functional CC cloning of genes encoding proteins or enzymes involved in proteolytic cleavage. The invention is based on the use of caspase expression CC cassettes comprising the coding sequence of a proteolytic cleavage site CC flanked by sequences encoding two caspase subunit, a fusion polypeptide comprising a first and a second caspase subunit, separated by a cleavage comprising a first and a second caspase subunit, separated by a cleavage containing fusion polypeptide is used to identify a mutant cell line deficient in an enzyme of interest and is also useful for diagnosis and containing fusion of a polypeptide (e.g. Cathepsin B or urokinase, controlled to superession of a polypeptide (e.g. Cathepsin B or urokinase, controlled to superession of a polypeptide (e.g. Cathepsin B or urokinase, controlled to superession of a polypeptide (e.g. Cathepsin B or urokinase, controlled to superession of a polypeptide (e.g. Cathepsin B or urokinase, controlled to the tumour cells). DNA encoding fusion
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase subunit, useful for cloning gene encoding enzymes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; caspase-8; MACH; FLICE; Mch3; cysteine protease; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human caspase-8 DNA
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2887 BP; 853 A; 595 C; 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 15; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteolytic cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAE00605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordell B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2000; 2000US-0225564
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                                                                                                                                                                    573 GATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTCTTTTATCTTTTGT
                                                            633 GTTTTTTTTCGAGCCATG
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                                                                                                                                                                                                                                                                                                     Similarity
GTTTTTTTCAAGCCCTG
                                                                                                                                    GATTCTGCCTTTCTGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGT
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                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used
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/product= "Human caspase-8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in gene therapy.
                                                                                                                                                                                                                                                                                                 10.7%;
                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                                                                                                 71.6;
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                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                         other;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                    0
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CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cantivity, and can be used in gene therapy and vaccine production. (I) CC arctivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic contents and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK85492 to AAK8793 and AAM82169 cranerase research executions and the areasent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding useful for preventing,
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            sequences used in the exemplification
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2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
2001US-0259678.
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2000US-0249208.
2000US-0249209.
2000US-0249210.
2000US-0249211.
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2000US-0249265.
2000US-0249297.
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2000US-0249300
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2000US-0246610
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2000US-0246532
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                                                                                                                                                                                                                                                                                                              human immune/hematopoietic antigen diagnosing and/or treating cancers
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          of the present
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AAM82169 invention

and

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                                                 Homo
                                                                                    MACH; MORT-1 binding protein; mediator of receptor toxicity; cell death; antibody; FAS ligand receptor; FAS-R; death domain region; septic shock; tumour necrosis factor; tumour, HIV-infection; oilgodendrocyte death; apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis; apoptosis/programmed cell death; p55-R; graft rejection; acute hepatitis; autoimmune disease; multiple sclerosis; AIDS-inhibited T-cell suicide;
                                                                                                                                                                    MACH isoform
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                                                                                                                                                                 alphal coding
                                                                                                                                                                                           (first entry)
           Location/Qualifiers 291..1731
                                                                                                                                                                                                                                              cDNA;
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94.4%;
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Pred. No. 7.6e-14
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RESULT 3
AAK77217 standard; DNA; 45017 BP.
XX
AC AAK77217;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen
XX
KW Human; immune; haematopoietic; immu
KW cytostatic; gene therapy; vaccine;
XX
PN W0200157182-A2.
XX
PN W0200157184664.
PN 11-MAX-2000; 2000US-0215135
PN 11-MAX-2000; 2000US-0215880.
PN 11-JUL-2000; 2000US-021647.
PN 11-JUL-2000; 2000US-021647.
PN 11-JUL-2000; 2000US-02168990.
PN 11-JUL-2000; 2000US-02168990.
PN 11-JUL-2000; 2000US-0224519.
PN 11-JUL-2000; 2000US-0224519.
PN 11-AUG-2000; 2000US-0224519.
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atic; gene therapy; vaccine; metastasis; ds.
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     14-SEP-2000
21-SEP-2000
21-SEP-2000
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22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
31-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
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14-AUG-2000;
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2000US-0231968.
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2000US-0232400.
2000US-0232401.
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2000US-0225266.
2000US-0225267.
 2000US-0237040.
2000US-0239935.
2000US-0249960.
2000US-0241785.
2000US-0241787.
2000US-0241787.
2000US-0241808.
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05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000

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                                                        GCATTTCAGCCACAGGGCTGACTTTACCCAGTCCGGCGGGAGGAGGAGAGAGGGCTGGTCT
                                                                                                                                      GTGACTTCAGTGCTGAGGTTTGATCAAGGCAAAGGGAAACTTCCTATTCCCAGACCCTTT
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nilarity 94.4%;
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Pred. No. 7.5e-1
0; Mismatches
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7.5e-148;
7.5e-30;
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25-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 03-OCT-2000 04-NOV-2000 08-NOV-2000 09-NOV-2000 09-NO

2000US-0244960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inactivation of a caspase-8 (CASP8) gene is determined by detecting a modification of CASP8 genomic DNA that results in inactivation of the gene. CASP8, a cysteine protease, is part of the death inducing signaling complex (DISC) associated with the Fas receptor. CASP8 is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASP8 promoter region sequences, in particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation. Methylation PCR can be used to examine even minute amounts of patient material to demonsrate whether the CASP8 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   death-receptor-mediated apoptosis in cells containing an inactivated CASP8 gene is also provided.
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670; Conser
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                              GTGGTGAAGTTTTCTCTTCTCTCGGAGACCAGATTCTGCCTTTACGCTGGAGGGAAGTG
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                                                                                   TGTTCGAGTGAGTCATCTCTGCTTCTGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCT
                                                                                                               TGTTCGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCT
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Pred. No. 3.5e-196;
; Mismatches 0;
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RESULT 2
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ID AAK77216;
XX AAK77216;
XX AAK77216;
XX AAK77216;
XX AAK77216;
XX AAK77216;
XX DT O7-NOV-200
XX Human; imm
XX Human; imm
XX Cytostatii
XX Cytostatii
XX Cytostatii
XX AAK7200
PM 09-AUG-200
XX 31-JAN-200
PM 04-FEB-200
PM 11-MAR-200
PM 07-JUN-200
PM 11-MAR-200
PM 11-MAR-200
PM 11-JUL-200
PM
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밁 δÃ 밁 Q Вb δÃ В Ωy В δÃ 멍 80 В γQ В δÃ D, δÃ

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14 AUG 2000

18 AUG 2000

22 AUG 2000

22 AUG 2000

23 AUG 2000

23 AUG 2000

01 SEP 2000
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen genomic sequence
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14-JUL-2000;
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4 ABL33869  4 ABC25138  ABQ25138  ABQ25138  ABQ25138  ABL5418  ABL5418  ABBN80019  ABL32217  ABL32217  ABSC8142  ABK28142  ABK28142  ABK28142  ABK28142  ABK28142  ABL70131  ABK28142  ABL70131  ABK31176  ABK31177  ABK31176  ABK31176  ABK31177  ABK31177  ABK31177  ABK31177  ABK31177  ABK31177  ABK31178  ABK31178  ABK31178  ABK31179  ABK	4 A	86		ω.	ω ω	
4 ABI33869  4 ABI33869  4 ABQ25138  ABQ25138  ABQ25138  ABL54318  Chemically treat  4 ABU25139  ABB32217  ABS45303  ABB80035  ABB80035  ABB80035  ABB25421  ABL322116  ABL32116	4	86		ω.	32	
4 ABI33869 4 ABI33869 5 ABQ25138 6 ABQ25138 6 ABQ25138 6 ABQ25138 6 ABRO25138 6 ABRO25138 6 ABRO25138 6 ABRO25138 6 ABRO25138 6 ABRO25139 6 ABRO2517 7 ABL32217 7 ABL32217 7 ABRO25139 7 ABRO25139 7 ABRO25131 7 ABRO2514 7	4	86		ω	31	
4 ABE33869  4 ABE33869  4 ABQ25138  6 Oligonuclectide  4 ABQ25139  6 Chemically treat  4 ABB32217  4 ABB32217  5 AAS45303  6 ABN80035  7 ABN80035  7 ABN80035  8 ABN8019  8 ABN8019  9 Human immune system in the sy	4	324	٠	34	30	
4 ABI33869  4 ABQ25138  ABQ25138  Oligonuclectide  4 ABQ25138  Oligonuclectide  4 ABU25138  Oligonuclectide  4 ABU35118  Chemically treat  4 ABN80019  4 ABU32217  ABU32217  ABU32217  Chemically prett  ABN80035  ABN80035  Human chemically  ABU20131  Chemically treat	4	24		ى 4	29	
4 ABL33869 Human immune sys ABQ25138 Oligonuclectide 4 ABQ25139 Oligonuclectide 4 ABL54318 Chemically treat 4 ABL8019 Human chemically 4 ABL32217 Human immune sys 2 AAS4503 Chemically pretry 4 ABL32217 Human chemically pretry 5 AAS4503 Human chemically pretry 6 ABS40315 Human chemically pretry 7 AAS40316 Human chemically 8 ABS40315 Human chemically	4	324	٠	34	28	
4 ABL33869 Human immune sys 4 ABQ25138 Oligonucleotide 4 ABQ25139 Oligonucleotide 5 ABL54318 Chemically treat 6 ABL32217 Human chemically 6 ABL32217 Chemically pretr 7 ABL3233 Chemically pretr 8 ABN845303 Human chemically 8 ABN845303 Human chemically	4	14		34	27	
4 ABE33869 Human immune sys ABQ25138 Oligonucleotide ABQ25139 Oligonucleotide Chemically treat ABM80019 Human chemically ABB32217 Human immune sys AAS45303 Chemically pretri	4	14	٠	34	26	
4 ABL33869 Human immune sys 4 ABQ25138 Oligonuclectide 4 ABQ25139 Oligonuclectide 6 ABQ25139 Chemically treat 6 ABL64318 Chemically treat 7 ABL860119 Human chemically 8 ABL32217 Human immune sys	2	14	٠	34	25	
4 ABL33869 Human immune sy 4 ABQ25138 Oligonucleotide 4 ABQ25139 Oligonucleotide 4 ABL54318 Chemically tree 4 ABN80019 Human chemical	4	51		34	24	
4 ABL33869 Human immune sy 4 ABQ25138 Oligonucleotided 4 ABQ25139 Oligonucleotide 4 ABL54318 Chemically tree	4	51		34	23	
4 ABE33869         Human immune sy           4 ABQ25138         Oligonucleotide           4 ABQ25139         Oligonucleotide	4	5	٠	34	22	
4 ABC25138 Human immune sy 4 ABC25138 Oligonucleotide	4	ω		34	21	a
4 ABL33869 Human immune sy	4	63		34	20	
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4 ABQ15813 Oligonucleotide	4	$\infty$		34.6	18	a
4 ABQ15812 Oligonucleotide	4	$^{\circ}$		4	17	
4 ABL33932 Human immune sy	4	ω		35	16	
1 AAA10595 Gene encoding a		74		35	15	a
2 AAK81668 Human immune/hae	N	25		35 5	14	
4 AAQ53209 Human cyclin D3	4	N			13	
2 AAF98635 Human ovarian ca	N	$\circ$		35.2	12.	a
3 ABV25186 Human prostate e	ω	2819	υ ω	35.4	11	
2 AAS46	2	Ġ.		36	10	

## CASP8; caspase-8; promoter; Region 1; inactivation; methylation; Cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; ss. Homo sapiens. CASP8 promoter Region 1. 31-OCT-2000 AAA51792; AAA51792 standard; DNA; 670 BP (first entry)

ALIGNMENTS

Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing prognosing cancer, comprises detecting a modification of genomic I Kidd WPI; 2000-452423/39. (SJUD-) ST JUDE CHILDREN'S RES 30-DEC-1999; 06-JUL-2000. WO200039347-A1 31-DEC-1998; Lahti JM, 98US-0114308 99WO-US31280 HOSPITAL.

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Oligonucleotide fo Oligonucleotide fo Human angiogenesis

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/note="AluSx repeat: matches 9. .290 of consensus AluSx repeat: matches 9. .290 of consensus AluSx repeat: matches 9. .290 of consensus" 13548. .13776
                                                                       /note="HERVL repeat: matches 1902. .2701 of consensus" 24949. .25225 /note="HERV16 repeat: matches 882. .1164 of consensus HERV16 repeat: matches 882. .1164 of consensus 25788. .26094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1 repeat: matches 3951 . .4433 of consensus"
15943 . .16022
/note="L2 repeat: matches 2664 . .2750 of consensus"
complement(16038 . .16616)
/note="match: GSS: Em:AQ541664"
17138 . .17193
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/note="LLME3A repeat: matches 5785. .5859 of consensus LIME repeat: matches 5785. .5859 of consensus"
15050. .15303
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                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LTR16C repeat: matches 56. .387 of consensus LTR16C repeat: matches 56. .387 of consensus" 21088. .21177 /note="FLAM_A repeat: matches 10. .99 of consensus FLAM_A repeat: matches 10. .99 of consensus 21469. .22143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT1C repeat: matches 1 .193 of consensus MLT1C repeat: matches 1 .193 of consensus" join(19542..19799,20379 .20477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18611..18904
/note="MITIC repeat: matches 193. .466 of consensus MLTIC repeat: matches 193. .466 of consensus"
18905...19230
                                                                                                                                                                                                       /note="HERVL repeat: matches 1902. .2891 of consensus" 23611. .24388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 78. .133 of consensus MIR repeat: matches 78. .133 of consensus"
                                                                                                                                                                                                                                                                         /note="HERVL repeat: matches 2953. .4189 of consensus HERVL repeat: matches 2992. .4228 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="dJ380B8.3 (a novel mRNA)"
/note="match: ESTs: Em:R79825"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Junu(<19542. .19799,20379. .>20477)
/gene="dJ380B8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSg repeat: matches 1..310 of consensus AluSg repeat: matches 1..310 of consensus" 19231...19419
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L1ME repeat: matches 5525. .5777 of consensus"
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IR repeat: matches 15. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ401011"
20155. .20184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="dJ380B8.3"
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15337. .15774
                       //orte="Alux repeat: matches 1. .307 of consensus alux repeat: matches 1. .307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                      note="HERV
                                                                                                                                                                                                                                                                                                                                                      note="HERVI repeat: matches 4644. .5045 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="15 copies 2 mer ac 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                 MERVI repeat: matches 4345.
21856
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163987 ACTAAGTTTTCAAGACCAGTATGTATTTTACACTTCCGGCATATGGCAGTTTGGAATAG 164045
                                                                                                                                                                                                                                      163927 TATTATTTCGATATGTAATAAAATATAAAGACTTATTAATAAGTCCTGTTACCTTTTTGGT 163986
                                                                                                                                                                                                                                                                                                      328 TATTATTACTAAATGGAGTCAGTATAAATGCTTTTCCAATAAAGCATGTCCAGCGCTCGGG 387
                                                                                                                         388 CTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTCTTCTGAATGGTTGGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ417969"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.3%; Score 42.2; DB 59.7%; Pred. No. 0.12; rative 0; Mismatches
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Search completed: July 11, 2003, 04:06:58 Job time: 2000 secs

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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512 GGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGTGAAGTTTTCTCTTTCTCTCGGAGACC
                                                                                                                                                                                                                                                                                              Submitted (28-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 20, 2000 this sequence version replaced gi:8573783.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL136307 186882 bp DNA linear PRI 01-AUG-2000 Human DNA sequence from clone RP3-380B8 on chromosome 6p24.1-25.3 Contains a gene encoding the protein Neuritin, which is involved in promotion of neurite outgrowth, a Pyruvate kinase (PKM2) pseudogene, a novel mRNA, 4 CpG islands, ESTs, STSs and GSSs,
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                       annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL136307.12 GI:8574124
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="RP23-10B21"
/clone_lib="RPCI mouse BAC library
/clone_lib="RPCI mouse BAC library
45169 c 45091 g 65176 t 1703
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/note="LIMA9 repeat: matches 4022. .4632 of con
LIMA9 repeat: matches 4022. .4632 of consensus"
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MIR repeat: matches 16. .236 of consensus"
                                                                                                                 MER33 repeat: 10364. .10771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /290. .7462
/note="MIR repeat: matches 71, .262 of consensus"
7357. .7462
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/note="MLT1D repeat: matches 14. .283 of con
MLT1D repeat: matches 14. .283 of consensus"
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/note="MIR repeat: matches 134.
12145. .12963
                                              MLT1G repeat: matches 10775. .10875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1MA9 repeat: matches 4632. .6308 of consensus L1MA9 repeat: matches 4632. .6308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .300 of consensus
AluSx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 77. .145 of con
MIR repeat: matches 77. .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="p24.1-25.3"
/clone="RP3-380B8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .186882
                                                                                                                                                                                                              /note="THE1B repeat: matches 1. .
THE1C repeat: matches 1. .371 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1MB3 repeat: matches 5281. .6174 of con
L1MB3 repeat: matches 5281. .6174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                    /note="MLT1G repeat: matches 65.
MLT1G repeat: matches 65. .512 o
                                                                                                                                                                  /note="MER33 repeat: matches 192.
                                                                                                                                                                                                            THEIC repeat: matches
                                                                                                                                                                                                                                                                                 /note="MER33 repeat: matches -9..192 of consensus
MER33 repeat: matches -9..192 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1MB8 repeat: matches 6029. .6173 of consensus L1MB8 repeat: matches 6029. .6173 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1M4 repeat: matches 5688. .5772 of consensus L1M4 repeat: matches 5688. .5772 of consensus"
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                                                                                                                                                                                                                                                                                                                                                      repeat: matches 2637. .2699 of consensus'
                                                                                                                                            matches
                                                                                                                                            192. .324 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .236 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .145 of consensus
                                                                       of consensus
                           .252 of consensus"
                                                                                                                                                                                                              .364 of consensus consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .283 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .505 of consensus
                                                                                                                                                                  .324 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6174 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .543 of consensus
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                                                                                                                  RESULT 14
AC079470/c
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Matches 149; Conserv
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Best Local
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                pieces.
AC079470
AC079470.1 GI:9964835
HTG; HTGS_PHASE2; HTGS
                                                                                   Mus musculus
                                                                                                   AC079470
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGTTTGTCAACTATGTTTTAATCTCTGATGAAACGTCTTCTTAAATCTTTTGTTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGCGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTCTTCTGAAT
                                                                                                                                                                                                       CTCCTTTTATCTTTTGTGTTTTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                        musculus
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                 HTGS_PHASE2; HTGS_DRAFT
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/note="match: GSS: Em:AQ475563"

/note="match: GSS: Em:AQ34959"

/note="match: GSS: Em:AQ349959"

complement(join(29378. 29596,32193.

/note="match: GSS: The AQ34959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ469605"
complement(29346. .29501)
/note="match: STS: Em:HSPE42F07"
complement(join(29371. .29506,32)
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24237. .24500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29724. .30076
/note="LIMC/D repeat: matches 5540.
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29035. .29346
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27846. .28076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSc repeat: matches 1.
25038. .25173
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RP23-10B21, 1
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Pred. No. 0.073;
0; Mismatches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 1.
                                                                                     WORKING
                                                                   linear
G DRAFT SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .293 of
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                                                                                   inear HTG 02-SEP-2000 SEQUENCE, 18 ordered
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AUTHORS
TITLE
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AUTHORS
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Consensus quality: 219485 bases at least Q30
Consensus quality: 220848 bases at least Q30
Consensus quality: 220848 bases at least Q30
Estimated insert size: 208000; agarose-fp estimation
Estimated insert size: 202587; sum-of-contigs estimation
Quality coverage: 10.31 in Q20 bases; agarose-fp estimation
Quality coverage: 9.63 in Q20 bases; sum-of-contigs estimation
**NOTE: This is a 'working draft' sequence. It currently
** consists of 18 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.

** This sequence will be replaced
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 223387)
DOE Joint Genome Institute.
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Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint
The Transistrate 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Joint Genome Institute Center Code: JGI
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Center clone name: RPCI-23_10B21
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121324
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24944; contig of 24944 by in length
25044; gap of unknown length
31043; contig of 5999 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of contig
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contig of 17972 bp in length
gap of unknown length
contig of 18703 bp in length
                                 g of 4709 bp in lef unknown length g of 2200 bp in lef unknown length g of 39810 bp in leg of 39810 bp in length
                                                                                                                                                                    f unknown length
g of 5050 bp in 1k
f unknown length
g of 3263 bp in 1k
f unknown length
g of 29600 bp in 1
g of 29600 bp in 1
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of 2987
unknown
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of 4709
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: _EMPL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone RP11-294H11 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP3-448K1 is at 137907 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oup. Further information can be found at tp://www.sanger.ac.uk/HGP/Chr6 11-294H11 is from the library RPCI-11.2 constructed by the group Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-294H11"
/clone_lib="RPCI-11.2"
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                                                                                                                                         8556. .8860 / The second of consensus of the second of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSq repeat: matches 134.
5803. .6023
                                                                                      complement(8906
                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6200
                                                                                                                                                                                                                                                                                                                                                                                                                               /note≖"match: GSS: Em:AQ524727"
complement(6414. .6688)
                                                                                      /note="LIMC4 repeat: matches 7502
complement(8906. .9376)
                                                                                                                                                                                                                                                                                                                                        /note="MER20 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5056. .6364
/note="Alux repeat: matches 1. .306
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     'note="match: GSS: Em:AQ434542"
                                                           note="match: GSS:
                                                                                                                                                                                                                                                                                      'note="HALl repeat: matches 60. .161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                    'note="match: GSS: Em:AQ564844"
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                                                                                                                                                                                                                                                              . 8555
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                                                                                                                                                                                                                             LIMC4 repeat: matches 6798. .7502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S: Em:AQ528743"
.6677)
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                                                                                                                                                                                                                                                                                                                                              .218 of consensus"
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                                                                                                                                                                                                                       /note="MER93
21714. 22010
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1MB6 repeat: matches 5159, 20372, .20760
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//note="AluSc repeat: matches 29...305 of consensus"
13930...14527
//note="AluSc repeat: matches 5706...6298 of consensus"
15521...15805
//note="AluSx repeat: matches 11...296 of consensus"
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/note="13 co
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/note="AluSg repeat: matches 1.
19791. .19897
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17806. .18234
  /note="match: GSS: Em:B85271"
23820. .24103
                                                                                /note="MER57B repeat: matches
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18721. .18966
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/note="Alujo repeat: matches 1. .308 of consensus"
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'note="HERV16 repeat: matches 1794. .2013 of consensus"
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                                                                                                                                            'note="MER93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MB6
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note="LOR1b repeat: matches 32.
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note="HERV16 repeat: matches 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="MER52A repeat: matches 1063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="HERV16 repeat: matches 1689.
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                                                                                                                                                                                                                       ייבאיז repeat: matches 19.
22019
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                                                                                                                                         repeat:
                                                                                                                                                                                               repeat: matches 1.
                                                                                                                                                                                                                                                                                                           repeat:
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                                                                                                                                                                                                                                                                                                                                                                         matches 5625. .6100 of consensus"
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                                                                                                                                            matches 136.
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                                                                                   296.
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                                                                                                                                                                                               .305 of consensus"
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AL390074
AL390074.1
                                                                                                                                                                                  AL390074
Human DNA
       Submitted (05-APR 2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 6, 2001 this sequence version replaced gi:13396608.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 138006)
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Direct Submission
together with a note of the overlapping clone name. Note that the
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bukay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., David, R., David, R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, B.A., David, M.L., Davis, C., Davy-Carroll, L., Dederich, B., Durbin, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
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Dorner, F., Scheiflinger, F. and Falkner, F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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3, *** SEQUENCING
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COMMENT

1132 1232 2721 2821

contig of 1131
gap of unknown
contig of 1489
gap of unknown
contig of 1521

bp in length

length

bp in length
length
bp in length

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Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R. J., Lu, L., Lucier, R., Luna, R., Ma, J., Lozado, R. J., Lu, Lucier, R., Luna, R., Ma, J., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Okedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., PyLL, D., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rulz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Warren, R., Washington, C., Watliaton, S., Walliamson, A., Wleczyk, R., Wooden, S., Wolfe, G., and Gibbs, R., Washington, C., Watlington, S., Weinstock, G., and Gibbs, R., Johnson, N., Nelson, D., Weinstock, G., and Gibbs, R., Johnson, N., Leon, D., Weinston, D., Washinston, D., Wa
                                                     * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* CONSISTS of 74 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 184700)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Molecular and Human Genetics, Baylor College of Medicin
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:20303182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulk,S., Hume,J., Jackson,L.E.,
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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
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as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye: 100% of reassembly program: Phrap; version 0.990329 Consensus quality: 120491 bases at least Q40 Consensus quality: 124431 bases at least Q30 Consensus quality: 127875 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: GREO Center clone name: CH230-35C18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
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JOURNAL REFERENCE AUTHORS

TITLE

TITLE JOURNAL

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SOURCE
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                                  2887 bp
H.sapiens mRNA for MACH-alpha-1
X98172
X98172.1 GI:1403318
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Sequence
AX134419
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                           cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteolytic cleavage
Patent: WO 0129232-A 15 26-APR-2001;
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                          death; MACH-alpha-1; protease
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                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                             /protein_id="CAC39526.1"
//protein_id="CAC39526.1"
//db_xref="01:14271066"
//translation="mdpssmltpdigqldsedlaslkflsldyiporkoepikdalmlfortografikellerinrldigegldsedlaslkflstkereslgypogragisark
forlogkrmldesnlsflkellerinrldltiytlutrkeemerelgypogragisark
rwhlygiseevsrselrsfkflloeeiskokldddmulldifiemekryilgegkldil
krvcaqinksllkiindyeefskerssslegspopefsugeelcgvmtisdspregdse
sotldkygdkskergcycliinunnfakarekvpklhsladrutritree
LHFEIKPHDDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAPIY
ELTSOFTGLKOPSLAGKPKVFFIQACGGDNYQKGIPVETDSEEOPYLEMDLSSPGTRY
IPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVNYEV
SNKDDKKNMGKOMPOPFTTLRKKLVFPSD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
292. .1731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product"
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1. .2887
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from Patent WO0129232
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Pred. No. 2.9e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                    I66494
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               GI:2724471
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633 GTTTTTTTTCGAGCCATG 650
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1 (bases 1 to 2887)

Boldin, M.P., Goncharov, T.M., Goltsev, Y.V. and Wallach, D.

Involvement of MACH, a novel MORTI/FADD-interacting protease, in Fas/APO-1- and TNF receptor-induced cell death

Cell 85 (6), 803-815 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-JUN-1996) D. Wallach, The Membrane Research & Biophysics, Rehovot 4 (bases 1 to 2887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-MAY-1996) D. Wallach, The Weizmann Institute, Membrane Research & Biophysics, Rehovot 76100, ISRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              head and neck carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mandruzzato,S., Brasseur,F.,
                                                                                                                                                                GATTCTGCCTTTCTGCTGGAGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTATCTTTTGT
                                                                                                  GTTTTTTTTCAAGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exp. Med. 186 (5), 785-793 (1997)
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                                                                                                                                                                                                                                                                                                     mutation recognized
7218 bp
14 from patent US 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="thymus" 292. .1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="MACH-alpha-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="triggers cell death"
/codon_start=1
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Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breckenridge, D.G., Nguyen, M., Kuppig, S., Reth, M. and Shore, G.C. The procaspase-8 isoform, procaspase-6L, recruited to the BAP31 complex at the endoplasmic reticulum proc. Natl. Acad. Sci. U.S.A. 99 (7), 4331-4336 (2002)
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                                       AF422925.1
                                                    AF42292
                                                               Homo sapiens procaspase-8L (CASP8) alternatively spliced.
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/db_xref="GI:191530"
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/db_xref="taxon:9606"
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Breckenridge, D.G., Nguyen, M.,
Direct Submission
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Breckenridge,D.G., Nguyen,M., Kuppig,S., Reth,M. The procaspase-8 isoform, procaspase-8L, recruit complex at the endoplasmic reticulum proc. Natl. Acad. Sci. U.S.A. 99 (7), 4331-4336
                                                                                               1 (bases 1 to 2887)
Wallach,D., Boldin,M., Goncharov,T.
Modulators of the function of FAS re
Patent: US 6399327-A 14 04-JUN-2002;
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VSNKDDKKNMGKQMPQPTFTLRKKLVFPSD"
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/db_xref="taxon:9606"
organism="unknown"
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Nat. Med. 6 (5), 529-535 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 982)
                                                           سا
                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 982)
Teitz,T., Wei,T., Valentine,M.B., Vanin,E.F., Grenet,
Valentine,V.A., Behm,F.G., Look,A.T., Lahti,J.M. and
Direct Submission
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AF210257
                                                                                                                                                                                                                                                                                                                                          Submitted (01-DEC-1999) Tumor Cell Biology, St. Research Hospital, 332 N. Lauderdale, Memphis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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/db_xref="taxon:9606"
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112; Conservative
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AF422926.1
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Direct Submission
Submitted (24-SEP-2001) Biochemistry, McGill University,
Promenade Sir William Olser, Montreal, PQ H3G1Y6, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 413)

Breckenridge,D.G., Nguyen,M., Kuppig,S., Reth,M. and Shore,G.

The procaspase-8 isoform, procaspase-8L, recruited to the BAP

complex at the endoplasmic reticulum

proc. Natl. Acad. Sci. U.S.A. 99 (7), 4331-4336 (2002)
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Mammalia; Eutheria; Primates;
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                                                                                                                                                   /note="caspase precursor; alternatively spliced"
/codon_statr=1
/product="procaspase=8"
/protein_id="AAL87629.1"
/protein_id="AAL87629.1"
/db_xref="GI:19401521"
/tdb_xref="GI:19401521"
/translation="MDFSRNLYDIGEQLDSEDLASLKFLSLDYIPORKQEPIKDALML
FORLQEKRMLEDSNLSFLKELLFRINRLDLLITYLNTRKEEMERELQTP"
187 c 96 g 115 t
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="1"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                /gene="CASP8"
                                                                                                                                                                                                                                                                                                               /gene="CASP8"
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                                                                                            16.2%;
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Pred. No. 3.9e
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VECTOR: pBACe3.6
NEIGHBORING CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-156B7; the clone sequenced to the right is RP11-536IIB, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-575C6; actual end is at base position 180955 of RP11-575C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping information for this clone was provided by Dr. John D. McPharson, Department of Genetics, Washington University, St. Louis MCD. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The
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3739. .386
/note="match to EST 4184. .4747
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553, _600
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3971. .4133
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1228
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192. .228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to Homo (NID:g13456766)"
                                                                            (NID:g11044285)"
                                                                                                                                                                    4041.
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/db_xref="taxon:9606"
/chromosome="2"
                                         /note="similar to
(NID:g12791503)"
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              GCAAGAAAGAATGGCATATTACTTGCCGCCGACAGGGGTTATTATTACTAAATGGAGTCA 348
                                                                         GTGACTTCAGTGCTGAGGTTTGATCAAGGCAAAGGGAAACTTCCCTATTCCCAGACCCCTTT 288
                                                                                                                    ACATTTCAGCTACAGGGCTGGCTTTACCCAGTCCGGCGGAGGAGGAGGAGGGCTGGTCT 159696
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5615. .5984
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4657. .5468
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Direct Submission
Submitted (20-APR-2001) G
University School of Medi
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Waterston,R.H.
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Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington
Submitted (07-NOV-2001) Department of Genetics, Wissouri 63108,
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Jun 7, 2001 this sequence version replaced gi:13677176.
                                                                                                                                                                                                                                                       Submitted (03-JUL-2001) Genome University School of Medicine, MO 63108, USA 8 (bases 1 to 181150)
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Direct Submission
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Submitted (07-JUN-2001) Genome Sequencing Center, Washing
University School of Medicine, 4444 Forest Park Parkway,
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University School of Medicine,
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Submitted (07-APR-1999) Genome
University School of Medicine,
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Mammalla; Eutheria; Primates;
1 (bases 1 to 181150)
Sulston, J.E. and Waterston, R.
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erston, R.H.
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------Summary Statistics
Center project name: H_NH0575C06
                                                                                    Center: Washington University Genome Sequencing Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION

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Matches 568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-FEB-2000) Shinji Hadano, Tokai Universi Institute of Medical Sciences; Bohseidai, Isehara, Ka 259-1193, Japan (B-mail:shinji@nga.med.u-tokai.ac.jp, Tel:+81-463-91-5095, Fax:+81-463-91-4993)
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Sequencing vector: M13; 48%
Sequencing vector: M13; 48%
Chemistry: Dye-primer ET; 48% of reads
Chemistry: Dye-terminator Big Dye; 44% of reads
Chemistry: Dye-terminator Big Dye; 44% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178616 bases at least Q30
Consensus quality: 178729 bases at least Q30
Consensus quality: 178811 bases at least Q20
Insert size: 174000; agarose-fp
Insert size: 174000; agarose-fp
Quality coverage: 15.3 in Q20 bases; agarose-fp
Quality coverage: 14.71 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
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Direct Submission
Submitted (10-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Aug 9, 2001 this sequence version replaced gi:9958173.
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Waterston, R.H.
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Mammalia; Eutheria;
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                                                       NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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      82839
82939
82838: contig of 82838 bp in length
82938: gap of unknown length
179216: contig of 96278 bp in length
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Primates;
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Sequencing Center

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Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    July 10, 2003, 22:21:06 ; Search time 1995 Seconds (without alignments) 9773.875 Million cell updates/sec
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670
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1: gb_ba:*
2: gb_htg:
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_pr:*
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em_htgo_hum:*
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em_htg_rod:*
em_htg_mam:*
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em_in:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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01634 01579 01579 07411		C00396 C10935 C12301 C12301 P00458 UMYH97 L35749 L35749	AF422926 AF422929 AF422929 AF422929 AF211527 AF2115	D B03898 C07401
1634 1579 1579 9078 6838	104753 Mus musc 026231 Mus musc 161742 Human DN 356914 Homo sap 0117302 Rattus n 090178 Homo sap	003966 HOMO 003966 HOMO 109352 HOMO 123019 Rattu 004581 HOMO 075004 HOMO 035249 HOMO 035244 HOMO	Homo sa Homo sa Homo sa Homo sa Sequenc Sequence Rattus Human D Homo sa Homo sa Homo sa Homo sa Homo sa Homo sa	escription B038981 Homo sap C007256 Homo sap

### ALIGNMENTS

REFERENCE AUTHORS		ORGANISM	SOURCE	SEGMENT	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AB038980S2	RESULT 1
1 Hadano,S., Yanagisawa,Y., Skaug,J., Fichter,K., Nasir,J., Martindale,D., Koop,B.F., Scherer,S.W., Nicholson,D.W.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	Homo sapiens DNA.	2 Of 6		AB038981.1 GI:12862688	AB038981	Homo sapiens gene for caspase-8, exon 3, exon 4.	AB038980S2 6502 bp DNA linear PRI 23-FEB-2001		

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APPLICANT: Effertz, Roger J.

APPLICANT: Hauge, Brian M.

APPLICANT: Hauge, Brian M.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping FILE REFERENCE: 38-10(52679)&

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US 09/754,853

PRIOR FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 09/760,427

PRIOR APPLICATION NUMBER: US 09/767,427

PRIOR APPLICATION NUMBER: US 09/768

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 4593

SEQ ID NO 868

LENGTH: 132

TYPE: DNA ORGANISM: Glycine max

US-09-969-373-868
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                                                                                                                                                                NAME/KEY: misc_feature
. LOCATION: 115, 127, 156, 160, 163,
. OTHER INFORMATION: n = A,T,C or G
US-10-066-543-2507
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US-10-066-543-2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вb
                                                                                                                                                                                                                                                                                                     APPLICANT: Durham, Margarita
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.553
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2507
LENGTH: 234
                                                                                Query Match
Best Local S
Matches 20
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Best Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2507, Application US/10066543 Publication No. US20030087818A1
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Local Similarity 87.0%;
hes 20; Conservative
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83 ATATATATATACATTGAAAAAA 105
                        3 ATATATCTACATTCAAAACAA 25
                                                                             Ch 72.8%; Score 18.2; DB 9; Similarity 87.0%; Pred. No. 7.3e+02; 20; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ATATATCTACATTCAAAACAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter, Darrick
Fanger, Gary R.
Smith, Carole L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xu, Jiangchun
Indirias, Carol Yoseph
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.2; DB 10;
Pred. No. 6.8e+02;
0; Mismatches 3;
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                                                                                                                     Length 234;
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Search completed: July 8, 2003, 06:04:42 Job time: 25.6593 secs

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; LOCATION: (2618, 2780)
US-10-239-676-78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-239-676-78/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: THERAPY OF BREAST CANCER FILE REFERENCE: MRI-049
CURRENT PAPPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR RILING DATE: 2001-07-18
NUMBER: OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13758
LENGTH: 4020
                                                                                                                                                                                                                                                                                              2000-09-01
NUMBER OF SEQ ID NOS:
SEQ ID NO 78
LENGTH: 6071
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Publication No. US20030082609A1
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Best Local Similarity
                                                                             Matches
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                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/EP01/03968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLEK, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                         OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                            Local
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10019173.8
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 3475
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                                       1 CCATATATATCTACATTCAAAACAA 25
                                                                                            Similarity
CAAAATATATTACATTCTAAACAA 3451
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                                                                                          74.48;
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84.0%;
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Pred. No. 7.5e+02
                                                                                          Score 18.6;
Pred. No. 7
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                                                                                            .9e+02
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RESULT

RESULT 14 US-09-969-373-868/c

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TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Soybean Cyst Nematode Resistance FILE REFERENCE: 38-10 (15610)B

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION UNMBER: US 60/174,880

PRIOR FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 1119

SEQ ID NO 2

LENGTH- 22-1
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, NAME/KDY: CDS
, LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-2
Дb
                                                   Query Match
Best Local Similarity
"~* hes 21; Conserv?
                                                                                                                                               ; NAME/KEY: CDS; LOCATION: (46798)..(48763).(48975)..(49573); OTHER INFORMATION: Clone ID: 240017_region_G3 US-09-754-853A-3
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US-09-754-853A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hauge, E
APPLICANT: Parnell
APPLICANT: Parsons
APPLICANT: Wang, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/754,853A CURRENT FILING DATE: 2001-01-05 PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                            LENGTH: 335913
TYPE: DNA
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TYPE: DNA
ORGANISM: Glycine
                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                          FEATURE:
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                     CCATATATATCTACATTCAAAACAA 25
CGATATATATACATAAAAAACAA 201137
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                                                                         Conservative
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                                                                                         74.4%;
                                                                                         Score 18.6;
Pred. No. 1.
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Pred. No. 1.1e+03;
                                                                         Mismatches
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                                                                                         DB 9;
L.1e+03;
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                                                                                                         Length 335913;
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RESULT 7
US-09-918-995-13475
Sequence 13475, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (1)...(487)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-13475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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US-09-745-763-12
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09745763 Patent No. US20020065394A1 GENERAL INFORMATION:
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Best Local :
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LENGTH: 487
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILTING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 CCATATATATATATCCAAGACAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 CCATATATATATATCCAAGACAA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCATATATATCTACATTCAAAACAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.4%;
Similarity 84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                      CITY: Cambridge
STATE: MA
                                                                                                                                                      ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                          OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                          Jacobs, Kenneth
                                                                                                                                                                                                                                                     Merberg, David
Treacy, Maurice
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                           Evans, Chery
                                                                                                                                                                                                                                                                                                                        LaVallie, Edward R.
Collins-Racie, Lisa A.
                                                                                                    U.S.A.
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                                                                                                                                                                                                                                                                                                                                                            John M.
                                                                                                                                                                                                                          ENCODING
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Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.6; DB 9;
Pred. No. 5.7e+02;
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                                                                                                                                                                                                                         PROTEINS AND POLYNUCLEOTIDES THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
 Version #1.30
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Db
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US-10-044-205A-21
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                                      RESULT 10
US-10-198-846-13758
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Sequence 13758, Application US/10198846 Publication No. US20030099974A1
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 3003
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Best Local Similarity
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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KAPELLER LIBERMANN, ROSANA
APPLICANT: BANDARU, Rajasekhar
TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Pro
TITLE OF INVENTION: USES Thereof
FILE REFERENCE: 10147-5201
CURRENT APPLICATION NUMBER: US/10/044,205A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242,428
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241,884
PRIOR APPLICATION NUMBER: US 60/241,884
PRIOR APPLICATION NUMBER: US 60/241,877
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/
FILING DATE: 18-Jun-2000
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                       21;
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                                                                                                                        CCATATATATATATCCAAGACAA 2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10044205A
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84.0%;
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84.0%;
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                                                                                                                                                                                                                      Score 18.6;
Pred. No. 7
                                                                                                                                                                                                       Mismatches
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GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao

Wang, Youzhen Steinmann, Kathleen

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; OTHER INFORMATION: Clone ID: 240017_region_G3__201115_11 US-09-754-853A-149
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US-09-754-853A-149
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US-09-960-352-374/c
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           GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Soybean Cyst Nematode Resistance FILE REFERENCE: 38-10(15810)B CURRENT APPLICATION NUMBER: US/09/754,853A CURRENT FILING DATE: 2001-01-05 PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR DATE: 2000-01-07 SEQ ID NOS: 1119 SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 877
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 149, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
SEQ
                                                                                                                                                                                                                                                 Sequence 374, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local S
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APPLICANT: Patrnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/760,427 PRIOR FILING DATE: 2001-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCATATATATCTACATTCAAAACAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.6; DB 9;
Pred. No. 5.2e+02;
0; Mismatches 4
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Pred. No. 5.1e+02;
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 355
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORWATION: Clone ID: 02-LIB34-005-Q1-E1-A9
US-09-960-352-374
                                                                                                                                                                                                                                                                                                                                                                                   US-09-18-995-9724
Sequence 9724, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
NAME/KEY: unsure
; LOCATION: (301)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 53-BOVMS1-006-Q1-E1-F2
US-09-960-352-12299
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US-09-960-352-12299/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12299
LENGTH: 392
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Best Local
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COTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bos taurus
                      NAME/KEY: misc_feature LOCATION: (1)...(469)
                                                                                 ORGANISM: Homo
                                                                                                              TYPE: DNA
                                                                   FEATURE:
                                                                                                                                ENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 74.4%;
Local Similarity 84.0%;
les 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 CCAAATAAATCAACGTTCAAAACAA 225
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84.08;
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Pred. No. 5.
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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length: 2000000000
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2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: ./cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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12 US-10-044-205A-21
12 US-10-198-646-13758
9 US-10-239-676-78
9 US-09-754-853A-2
10 US-09-754-853A-3
10 US-09-969-373-868
9 US-10-239-676-43-2507
110 US-09-969-373-61
110 US-09-969-373-63
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US-09-754-853A-149
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             Sequence 877, App
Sequence 149, App
Sequence 374, App
Sequence 12299, A
Sequence 13475, A
Sequence 13475, A
Sequence 13, App1
Sequence 13, App1
Sequence 78, App1
Sequence 3, App1
Sequence 3, App1
Sequence 868, App
Sequence 61, App
Sequence 62, App1
Sequence 62, App1
Sequence 63, App1
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Sequence 663, App	Seguence 7547, Ap	663,	Sequence 7081, Ap	e 180	Sequence 180, App	8291	8290	Sequence 8289, Ap	Sequence 7640, Ap	7639		Sequence 1640, Ap	Sequence 13372, A	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 34, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 5147, Ap	Sequence 147, App	Sequence 363, App	Sequence 179, App		

#### ALIGNMENTS

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US-09-380-773-2/c

Sequence 2, Application US/09380773

Publication No. US20030113884A1

GENERAL INFORMATION:
APPLICANN: Helpi, Sike
APPLICANN: Schind, Brigitte
APPLICANN: Schindhel, Alexander
APPLICANN: Schindhel, Alexander
APPLICANN: Schindhel, Alexander
TITLE OF INVENTION: Methods for the Biosynthesis of Polyesters
FILE REFERENCE: MOBT136---118899.0136.NBUS00

CURRENT APPLICATION NUMBER: PCT/US97/03994

PRIOR APPLICANTON NUMBER: PCT/US97/03994

PRIOR FILING DATE: 1997-03-03

CURRENT FILING DATE: 1997-03-03

ILENGTH: 7120

TYPE: DNA

COSTURARE: Patentin version 3.0

SEQ ID NOS: 2

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

OUETY MATCH
ORGANISM: Clostridium kluyveri

US-09-380-773-2

OUETY MATCH
ORGANISM: CLOSTRIDIUM SCORE 19.2; DB 9; Length 7120;
Best Local Similarity '87.5%; Pred. No. 4 9e+02;
Matches 21; CONSETVATION ST. PRED. No. 4 9e+02;
MATCHE NO. 4 9e+02;
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OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION NUMBER: US/08/961/527

FILING DATE:
CLASSIFICATION UNMBER: US/08/961/527

FILING DATE:
PRIOR APPLICATION ACAM:
APPLICATION NUMBER: BB40P1

FILING DATE:
APPLICATION NUMBER: BB40P1

FILING DATE:
APPLICATION NUMBER: BB40P1

FILENDATE: NAME: BS70Nes; A. Anders
REGISTRATION NUMBER: BB40P1

FERENCE/DOCKET NUMBER: BB40P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504

TELECAX: (301) 309-8504

TELECAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 3652 base pairs
TYPE: nucleic acid
STRANDENDESS: double
TOPOLOGY: linear
US-08-961-527-251

Query Match
Best Local Similarity 80.0%; Pred. No. 1.6e+02:
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps

Qy 1 CCATATATATCTACATTCAAAACAA 25

Qy 1 CCATATATATCTTACATTCAAAACAA 25

Db 2085 CCATAAATATCTTGATTAAAATCAA 2109

Search completed: July 8, 2003, 05:57:14

Job time: 22.9955 secs
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RESULT 13
US-09-315-444-115
; Sequence 115, Application US/09315444A
; Patent No. 6232070
; Patent No. 6232070
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Best Local :
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                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
                                                                                                                                                                                                                                                                                                                                        NAME: Ginmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stodola, Robert TITLE OF INVENTION: No. 6348328el Compounds NUMBER OF SEQUENCES: 552
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 09-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                ENGTH:
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                                                                                                                                                              Similarity 20; Conserv
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Knowles, David
Nicholas, Richard
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80.0%;
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Pred. No. 1.
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Pred. No.
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                                                                                                                                                          1.6e+02;
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1.3e+02;
                                                                                                                                                                                        Length 945;
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CURRENT APPLICATION NUMBER: US/09/188,579

CURRENT FILING DATE: 199-05-20

PRIOR APPLICATION UNMBER: US/09/188,579

PRIOR FILING DATE: 1998-11-09

NUMBER: US/09/188,579
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                                                                                                                                                                                                                                                                                       RESULT 15
US-08-961-527-251
                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Nucleotide sequence of cap methyltransferase gene US-09-721-362-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-721-362-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/721,36:
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 09/315,444
PRIOR FILING DAYE: 1999-05-20
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 115
LENGTH: 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                  Sequence 251, Application US/08961527 Patent No. 6420135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 115, Application US/09721362
Patent No. 6420163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albacans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Candida albacans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                     COUNTRY:
                                                                                        CITY: Rockville
STATE: Maryland
                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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es 20; Conservative
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20; Conserv
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                                                   20850
                                                                      Maryland
{: USA
                                                                                                                          9410 Key West Avenue
                                                                                                                                                                                                                    Charles Kunsch
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                                                                                                                                             Human Genome Sciences,
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Pred. No. 1.6e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 4;
Pred. No. 1.6e+02;
D; Mismatches
                 inch, 1.4Mb storage
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RESULT 10
US-09-134-001C-2219/c
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US-09-054-298-17
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Sequence 2219, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.8
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 95
SOFTWARE: FASCED for Windows 02.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,655
FILING DATE: 14-MAR-1997
CLASSIFICATION 1514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE FORCET NUMBER: 34,819
REFERENCE TO COURSE NUMBER: 34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                STRANDEDNESS: bo
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No. 6258
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MEDIUM TYPE: Diskette
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ZIP: 02110-2804
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CITY: Boston
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                  nucleic acid
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86.4%;
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Pred. No. 1.4e
0; Mismatches
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Pred. No. 1.4e+02;
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1.4e+02;
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 2219
LENGTH: 342
TYPE: DNA
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US-08-966-316-6/c
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OPERATING SYSTEM: DOS
SOFFWARE: FESTSEM: FOF WINDOWS VERSION 2.
CURRENT APPLICATION NUMBER: US/08/966,316
FILLING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 35,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2111 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reddy, Roopa
APPLICANT: Murry, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                 TOPOLOGY: Line
                                                  TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                 TELEFAX:
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les 19; Conserv
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                                                                                                                                                                 650-845-4166
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BRSTNOT04
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Pred. No. 1.4e+02;
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US-09-128-155-16
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                                                                                                                                                                                                                                                                                                                                 Sequence 17 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER STLING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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Patent No. 6117654
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Best Local (
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
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ZIP: 02110-200.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
                                                                                                                                         STREET:
                                                                                     COUNTRY: USA
ZIP: 02110-2804
                                                                                                                          STATE:
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20; Conserv
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Similarity 83.3%;
20; Conservative
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5767262
                                                                                                                                         Boston
                                                                                                                        MA
                                                                                                                                                          225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.6; D
Pred. No. 88;
0; Mismatches
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Pred. No. 93;
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us-09-054-298-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                               OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,298
FILING DATE: 02-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ph.D. Ingrid A.
REGISTRATION NUMBER: P-42,306
REGISTRATION NUMBER: 08433/022002
                                                               TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                             SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 I
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                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FISH & .... STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fraser, Janis K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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STRANDEDNESS:
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Haber, Edgar
Jain, Mukesh
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N: 514
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Pred. No. 1.
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; INDIVIDUAL ISOLATE:
US-08-687-080-76
                               US-08-487-826B-13
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                                                  RESULT 4
                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (183)...(5957)
US-09-853-768-3
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF HELICASE-MOI EXPRESSION
FILE REFERENCE: RISS-0217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.8%;
Best Local Similarity 87.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 4600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0860

TELEPHONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09853768 Patent No. 6444466
                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
LENGTH: 7037
                                                                                                                                                               Matches
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/853,768
CURRENT FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 91
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                               Local Similarity
les 20; Conserv
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                                                                                                 1042
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                                                                                                                            3 ATATATCTACATTCAAAACAA 25
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                                                                                                 ATATATCTGTACATTCAAAAGAA 1064
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0N: 435
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26-JAN-1996
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Pred. No. 5
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Pred. No. 55;
                                                                                                                                                             Mismatches
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Sequence 1, Application US/09345217

Patent No. 6269142

GENERAL INFORMATION:

APPLICANT: DUFF, GORDON W.

APPLICANT: COX, ANGELA

APPLICANT: COX, ANGELA

APPLICANT: COX, ERRNCESCO S.

APPLICANT: DIGIOVINE, FRANCESCO S.

TITLE OF INVENTION: WITH AN IL-1 INFLAMMATORY HAPLOTYPE

FILE REFERENCE: MSA-010.02

FULE REFERENCE: MSA-010.02

CURRENT FILING DATE: 1999-06-30

EARLIER APPLICATION NUMBER: PCT/GB99/01481

EARLIER APPLICATION NUMBER: 9711040.7

EARLIER APPLICATION NUMBER: 9711040.7

EARLIER FILING DATE: 1997-05-29

NUMBER FILING DATE: 1997-05-29
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                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-345-217-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: IStaelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 8/.v
Thes 20; Conservative
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APPLICANT: Su, Xin-zl
APPLICANT: Wellems, T
TITLE OF INVENTION: F
TITLE OF INVENTION: R
NUMBER OF SEQUENCES:
SOFTWARE: PatentIn Ver. 2.0
                   NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CI
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STREET: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller, Louis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sim, Kim L.
Chitnis, Chetan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.8%;
87.0%;
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Pred. No. 55
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16th Floor
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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BG
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                                                                                                                                                                seq length: 0 seq length: 2000000000
    Issued_Patents_NA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1
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25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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ALIGNMENTS	US-08-257-073-2	US-09-252-816A-7	US-08-961-527-95	US-09-056-285A-3	US-08-791-347-16	US-08-822-999-10	US-09-221-017B-324	US-08-187-453-35	US-08-135-511-35	US-09-134-001C-1206	US-08-724-394A-22	US-08-724-394A-21	US-08-724-394A-20	US-09-657-474-7	US-09-268-992-7	US-09-851-896-3	US-09-410-464-13	US-09-349-677-3
	Sequence 2, Appli	Sequence 7, Appli	Sequence 95, Appl	Sequence 3, Appli	Seguence 16, Appl	Sequence 10, Appl	Sequence 324, App	Sequence 35, Appl	Sequence 35, Appl	Sequence 1206, Ap	Sequence 22, Appl	-	Sequence 20, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 3, Appli	Sequence 13, Appl	Sequence 3, Appli

#### RESULT 1 US-09-280-116-82 US-09-280-116-82 Sequence 82, Application US/09280116A Patent No. 6331427 GENERAL INFORMATION: APPLICANT: Robison, Keith E. TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Profile Reference: 5800-24, 035800/176965 CURRENT APPLICATION NUMBER: US/09/280,116A CURRENT FLING DATE: 1999-03-26 NUMBER OF SEQ ID NOS: 268 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 82 LENGTH: 798 TYPE: DNA ; FEATURE: nisc\_feature NAME/KBY: misc\_feature LOCATION: (1)..(798) OTHER INFORMATION: n = US-09-280-116-82 Query Match Best Local S Matches 21 OTHER INFORMATION: matrix metalloproteases FEATURE: ORGANISM: Homo sapiens Similarity 74.4%; nilarity 84.0%; Conservative ω, ŗ Score 18.6; D Pred. No. 40; 0; Mismatches Ω or DB 4. Length 798; Protease Homologs

: Sequence 76, Application US/08687080
Patent No. 5965427
; GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Ge
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:

RAD50 Gene

and Methods

of Use

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Sui CITY: Palo Alto STATE: CA COUNTRY: USA CIP: 94306

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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, 2 yoosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Direct Submission
Souclet, J.L., Aiglé, M., Artiguenave, F., Blandin, G., Bolottin-Fukuhara, M., Bon, E., Brottier, P., Casregola, S., de-Monting, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
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Saccharomycetales; Saccharomycetaceae; Pichia.
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2 rue Gaston Cremieux, CP 5706, 91057 EVEV cedex, FRANCE. (E-mail:
3 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, 29ossaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and varrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to Saccharomyces cerevisiae ORF YIL123w SIM1; involved in cell cycle regulation and aging | Similar to Saccharomyces cerevisiae ORF YKR042w [ UTH1 to the content of the co
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/strain="CBS 7064"
/db_xref="taxon:4920"
/clone="AX0AA030D10"
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95.2%;
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                                                                                                                                                                                                                  Score 19.4;
Pred. No. 1.
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Other_GSS: RPCIII-1217.TV
Other_GSS: RPCIII-1217.TV
Contact: Shaying Zhao, William Nierman, MacDepartment of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 200
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296
                                                                                                                                      Genomic exploration of the hemiascomycetous yeasts: yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                   Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Belottin-Fukuhara, M., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Durrens, P., Lepingle, A., Neuveglise, C., Durrens, P., Lepingle, A., Neuveglise, C., Durrens, C., Casaregola, S., Casaregola, C., Casaregola, S., Casaregola, S., Casaregola, C., Casaregola, S., Casaregola, C., Casaregola, S., Casaregola, C., Casaregola, C., Casaregola, C., Casaregola, S., Casaregola, C., Casaregola, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS06URI 849 bp DNA linear GSS 06-JUL-2001
T3 end of clone AX0AA012F02 of library AX0AA from strain CBS 7064
of Pichia farinosa, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tlgr.org/tdb/humgen/bac_end_search/bac_end_search.html Seg primer: SP6
   de Montigny, J., Spehner, C., Souciet, J.,
Wincker, P., Artiguenave, F. and Potier, S.
                                                                                                                                                                                                                                    Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pichia farinosa.
Pichia farinosa
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL416212.1
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1 (bases 1 to 651)
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/db_xref="GDB:7546278"
/db_xref="taxon:9606"
/clone="RPCI-11-12117"
/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
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                            Tekaia, F., Dujon, B.,
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2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
5 seqref(genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipplytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T3 end of clone AXOAAO30H08 of library AXOAA of Pichia farinosa, genomic survey sequence. AL418347.1 GI:12200957
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Cassaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                  Genomic exploration of the hemiascomycetous yeasts: yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)
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                                                                            Genomic exploration of the
                                                                                                     de Montigny,J., Spehner,C., Souciet,J.,
Wincker,P., Artiguenave,F. and Potier,S
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Direct Submission
FEBS Lett.
20584725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pichia farinosa.
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/clone="AXOAA012F02"
/clone_lib="AXOAA"
/note="end : T3"
a 167 c 150 g ;
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/strain="CBS 7064"
                      487 (1), 87-90 (2000)
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95.2%;
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Pred. No. 1
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library AXOAA from strain CBS 7064
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                                                                                                                               Tekaia, F.,
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    A set of

    Pichia

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de Jong, P. and Venter

linear

GSS 16-OCT-2000 RPCI-11-79F2,

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JOURNAL
REFERENCE
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ORGANISM
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CNS04K6T/c
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115P02 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon. 1 (bases 1 to 793)
1 (bases 1 to 793)
1 (bases 1 to 793)
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21; Conservative
                                                                                                                                                                                                                                                               This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouneau,L., Billault,A., Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS04K6T
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                                                                                                                                                                                                                                                                                                                                                                         Genoscope.
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                                      Conservative
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/strain="TQ100DH3"
/db_xref="taxon:3712"
/clone="BOMHQ23"
/clone="BOMHQ23"
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Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
a 140 c 171 g 230 t
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/db_xref="taxon:99883"
/clone="115902"
/clone_lib="G"
/note="Genoscope sequence ID : COB
94 c 208 g 240 t 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                793 bp DNA linear GSS 21-MAY-2000 nigroviridis genome survey sequence T7 end of clone library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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91.3%;
                                                   79.2%;
84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                   Score 19.8; DB Pred. No. 1e+03; 1; Mismatches
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                                                                                                                      COBG115DH01LP1~end : 31 others
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                                                                    Length 793;
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SOURCE
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AZ519839/c
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AQ342956/c
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                                                                                                                                                                                                                                 269 ATATATATGTACATTCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other_GSSs: RPCIII-79F2.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ519839
RPCI-11-79F2.TVB
                                                                  DNA sequence.
AQ342956
AQ342956.1 G
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 513)
                                                                                                                                                                                                                                                                     3 ATATATATCTACATTCAAAAC
                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC end sequences of library RPCI-11 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
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RPCI11-12117.TJ
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20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      /ceil_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_
/note="Vector: pBACe3.6; Site_
RPCIII Human Male BAC Library"
1 65 c 76 g 203 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:7530073"
/db_xref="taxon:9606"
/clone="RPCI-11-79F2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-11"
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95.2%;
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EcoRI; Site\_2:

ECORI;

others

Indels Length

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0,

linear

GSS 07-MAY-1999 RPCI-11-12117,

Euteleostomi;

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AA966215/c
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Best Local S
Matches 21
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Emericella nidulans.
Emericella nidulans
Eukaryota; Fungi; Ascomycota;
Eurotiales; Trichocomaceae; Em
1 (bases 1 to 371)
                                                                                                                                                                                                                                                                                                                                                                                         Email: broe@ou.edu
We anticipate the future release
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Chemistry and Biochemistry Advanced Center for Genome Technology, Un 620 Parrington Oval, Norman, OK 73019, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 405 325 4912 Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Bruce A. Roe, University of Oklahoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An Aspergillus nidulans EST Database Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W.,
Prade,R. and Roe,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCATATATATCTACATTCAAAACAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA966215.1
                                                  Similarity
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CATATATATCTACATTCAAAACA 24
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                                 Conservative
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                                                                                                                   /clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library" /tissue_type="vegetative mycelia, asexual structures" /note="vector: pBlueScript SK-; Site_1: EcoRI; Site_2: xhoi; 5 end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript" 3' end of cDNA cloned into XhoI site of pBluescript" 1 60 c 106 g 76 t
                                                                                                                                                                                                                                             /organism="Emericella nidulans"
/strain="FGSC A26"
/db.xref="raxon162425"
/clone="v4e09a1"
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/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
/note="Male adult, hematopoietic tissue, stem cell"
/s4 c 57 g 140 t 10 others
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/db_xref="taxon:9606"
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                                                                                                                       1 (bases 1 to 764)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSS: BOWHQ23TR
                                                                                                                                                                                    Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosid; I; Brassicales; Brassicaceae; Brassica.
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Seq primer:
Class: shear
                         Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ATATATCTACATTCAAAACAA 25
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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BJ401889.1 GI:19314806
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: 301-838-3523
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 sheared ends
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Location/Qualifiers
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65 c 70 g 2:
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/clone="dds19a20"
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                                                                                                       Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shipata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Teunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, T., Yuonoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, Y., Watanatsu, M., And Hayashizaki, Y., Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihde Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 582)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission
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AL737904
AL737904.1 GI:21344543
GSS
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This sequence was generated from the T7 end of
part of the Daniokey Pilot BAC Library created
                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 318)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB404480 mRNA linear EST 15-JUL-2000 BB404480 RIKEN full-length enriched, ES cells Mus musculus cDNA cione C330036108 3', mRNA sequence.
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Location/Qualifiers
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
Tel: 81-45-503-9222
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86 c 101 g 204 t
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/db_xref="taxon:7955"
/clone="DKey-1P18"
/tissue_type="Testis"
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by R. Plasterk
                         230-0045, Japan
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
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D62159.1
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                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 369)
1 (bases 1, Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M. Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaich, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H.,
                                                                                                                                                                                                                                                                                                                                                                                  D62159 369 bp mRNA linear HUM242G12B Clontech human aorta polyA+ mRNA (#6572) CDNA clone GEN-242G12 5', mRNA sequence.
Shin,S. and Nakamura,Y.
Fujiwara et al. (1995)
Unpublished (1995)
Contact: Tsutomu Fujiwara
                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="ES cells"
/lab_host="SOLR"
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/clone="C330036I08"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                           Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithGemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, T.P.I., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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148797 MARC 4BOV Bos taurus
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Class: BAC end
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Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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BACKWARD: GTTTTCCCAGTCACGACG
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DH10B"
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
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/db_xref="taxon:7668"
            Library made from pooled tissue embryos."
                                                                                     /clone_lib="MARC 4BOV"
/tissue_type="pooled"
                                                       /note="Vector:
                                                                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                  /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 236 row: A column: 11
Seq primer: SP6
Class: BAC ends.
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Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
                 1 CCATATATATCTACATTCAAAAACAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPC1-24-336A11"
/clone_1ib="RPC1-24"
                                                                                                                                                          /cell_type="Spleen/Brain" /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; APCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                            /sex="Male"
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Pred. No. 7.1e+02;
0; Mismatches 3;
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 81.6
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# ALIGNMENTS

AZ149876/c
AZ149876
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AZ149876
DEFINITION
SP\_0048\_B2\_F0l\_T7 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic ACCESSION
AZ149876
VERSION
AZ149876
VERSION
AZ149876
Strongylocentrotus purpuratus
SUURCE
ORGANISM
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euchinoidea; Etrongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Strongylocentrotus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Echinocentrotus
Strongylocentrotus
I (bases 1 to 504)
I (bases 1 to 504)
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray
G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and
HOOD, L.

MEDLINE
CONTACT: Cameron, RA, Davidson, EH, Hood, L
CONTACT: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 793-3047

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) cannot acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) croteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prove to diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cc cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54920 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2000

06-DEC-2000

08-DEC-2000

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11-DEC-2000
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17-NOV-2000;
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P-PSDB; AAM88893.
                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA,
                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0251856.
2000US-0251868.
2000US-0251869.
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2000US-0251990
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2000US-0251479
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2000US-0251988
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2000US-0250160
                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM;
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Query Match Best Local Similarity

74.48; 84.08;

Score 18.6; DB 22; Pred. No. 3.3e+02;

Length 379;

Sequence 379 BP;

108 A; 62 C; 104 G; 101 T; 4 other;

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Matches
21;
Conservative
0
Mismatches
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Search completed: July 8, 2003, 03:11:19 Job time: 27.9421 secs

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209 CCACATATATCTTCATTAAAAACCA 185

CCATATATATCTACATTCAAAACAA 25

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RESULT 15
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Matches 21
                                                                                                                                                                                                                                                      31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
 17-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire production at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                            28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .674/c
AAK61674 standard; cDNA; 379 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 361 BP; 100 A; 52 C; 73 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 CTATATATTTTTCATTCAAAAAAA 151
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21; Conservative
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   2000US-0179065
2000US-018466A
2000US-018466A
2000US-018974
2000US-0199076
2000US-0199076
2000US-0205515
2000US-0209467
2000US-0214886
2000US-0214886
2000US-0214880
2000US-0216880
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2000US-0216880
2000US-0217487
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Pred. No. 3.3e+02;
0; Mismatches 4
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    14-AUG-2000
14-AUG-2000
114-AUG-2000
12-AUG-2000
22-AUG-2000
22-AUG-2000
22-AUG-2000
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23-AUG-2000
21-SEP-2000
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21-SE
2000US-0234274
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2000US-0234294
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2000US-0236369
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0237037
2000US-0247186
2000US-0241787
2000US-0241787
2000US-0241786
2000US-0244776
2000US-02464776
2000US-02464776
2000US-02464778
2000US-02465236
2000US-02465236
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2000US-0225757.
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2000US-0225759.
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2000US-0226868.
2000US-0227182.
2000US-0227182.
2000US-0227009.
2000US-0228924.
2000US-0229287.
2000US-0229387.
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RESULT 13
AAI61518
ID AAI61
XX AAI61
AC AAI61
AC AAI61
XX Soybe
XX Soybe
KW Soybe
KW SCN r
KW SCN r
KW SQU 24001
XX W0200
XX W0200
XX 19-JU
PP 05-JA
XX 07-JA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirhelmatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9905 BP; 3133 A; 75 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 35; 32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
              07-JAN-2000; 2000US-0174880
                                          05-JAN-2001; 2001WO-US00552
                                                                                                 WO200151627-A2
                                                                                                                            Glycine
                                                                                                                                                                                  Soybean; antihelmintic;
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                                                                                                                                                      bean; antihelmintic; gene therapy; soybean cyst nematode;
resistance; rhg1; Rhg4; SCN resistant allele; plant breed
017 region G3; 318013 region A3; 515002 region G2; ds.
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.8;
Pred. No. 3
                                                                                                                                                                                                               SEQ ID NO: 149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1920 G; 4777
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      8; DB 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                        plant breeding;
G2; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences
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RESULT 14
AAS1681/c
ID AAS1916
XX AAS1916
AC AAS1916
XX O6-NOV
DT 06-NOV
XX Human;
KW Vaccin
KW Vaccin
KW tissue
KW nervou
XX Nervou
XX Homo s
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Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an ringl or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                           Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI91681 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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          Claim 1; SEQ ID
                                    disorders
                                                                                                                                                                                                                                             07-SEP-2001
                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                      nervous system disorders; arthritis; inflammation; ss
                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001 (first entry)
                                                diagnosing
                                                                                                                                                                             28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                     WO200164835-A2
                                                                                                                                                                                                                   26-FEB-2001;
                                                           Isolated nucleic
                                                                                                                                                  (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           purified nucleic acid for nematode resistance and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-425872/45
                                                                                      2001-514838/56
DB; AAO11750.
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                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATATATCTACATTCAAAACAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the specification.
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                                                                                                                           Liu
                                               and.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                             2000US-0515126
2000US-0577409
                                                                                                                                                                                                                   2001WO-US04927
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                                                treating
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            Ö
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                                                            acids
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84.0%;
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         1399pp + Sequence Listing;
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                                                polypeptides,
g. leukaemia,
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Pred. No. 3.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                      11741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a soybean plant having soybean plant breeding programs -
                                                useful for prinflammation
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                                                for preventing tion and immun
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antiasthmatic;

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RESULT 10
ABL33519/c
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ABL32705/c
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Best Local S
Matches 21
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Best Loc
Matches
                                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, newofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
01-SEP-2000;
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                          Nucleic acid comprising for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                      01ek
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                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL33519;
                                                                                                         Local
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                                                                                                       Similarity
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                                                                                                                                                                                                                                                                          SEQ
                                                                                                                                                                                                                                                                                                methylation
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                                                                                            Conservative
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2000DE-1043826
                                                                                                                                                                                                                                                                          ID NO 1492;
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                                                                                                                                          B₽;
                                                                                                                                                                 present sequence
                                                                                                                                        1725 A;
                                                                                                                                                                                                                                                                                                          treatment
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                                                                                                     75.2%;
90.9%;
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87.5%;
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                                                                                                                                                                                                                                                                                                          fragment of chemically modified gene, useful nent of diseases associated with abnormal
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                                                                                                                                                                                                                                                                         32pp + Sequence Listing;
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                                                                                                                                         36 C; 1004 G; 2753 T;
                                                                                            0;
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Pred. No. 2.1e
0; Mismatches
                                                                                          Score 18.8; D
Pred. No. 2.9e
0; Mismatches
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                                                                                                       9e+02;
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                                                                                                                                         N
                                                                                                                                                                 invention.
                                                                                                                                         other;
                                                                                                                                                                                                                                                                         German.
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                                                                                            Indels
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                                                                                                                             ABL32062,
                                                                                                                                        RESULT
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Best Local
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                                                                                                                                                                                                                                                                                    can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
          Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                             Human
                                                                                           ABL32062
                                                                                                                ABL32062 standard;
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 678; 32pp +
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01-SEP-2000;
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                                                                                                                                                                                                                                                                      6297 BP; 1577 A; 217 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock
                                                                                                                                                                                                                                                                                                                                                               invention provides a number of human immune system associated are modified by the methylation of cytosines. The sequences
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2000DE-1043826
                                             system associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system associated gene
                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system disease; cytosine methylation;
                                                                                                                 DNA;
                                                                  entry)
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90.9%;
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                                                                                                                                                                                                                                    Pred.
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NO:
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                                                                                                                                                                                                                                                                     0 other;
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i gene, us 1 abnormal

useful

6297; 0

Gaps

0

neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

bowel

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cc bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since cc numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CPG dinucleotides and may CC cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and cor therapy of existing diseases or the predisposition to specific compared to another set of genetic and/or epigenetic parameters may be compared to another set of genetic and/or epigenetic parameters, the CC differences serving as basis for diagnosis and/or parameters, the care disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor cancer cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
AAS46544/c
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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diseases.
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                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                                                                      analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
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; tumour; CpG dinucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               suppressor gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATATATATCTACATTCAAAACAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylation;
                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d arthritis,
The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                      of chemically modified genes associated with tumour oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state
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2000DE-1019058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thritis, psoriasis and inflammatory/ulcerative present sequence is a gene of the invention.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemically modified sequence
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No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                            state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4654;
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                                                                                                                                                                                                                                                                                                                                                                                                          e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                          suppressor
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Sequence 15373

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ABL32466/c
ID ABL32466 standard;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epil neurofibromatosis; rheumatoid arthritis nooringis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncogenes. Sequences with even numbered Seq complementary sequence of the corresponding ID 2 and ID1, ID 536 and ID 535, except for is missing).
                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8845
                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                      30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                             Nucleic acid comprising for diagnosis and treatment cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                            WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                    Claim 1;
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                                                                                                                                                                                                                                     ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         bromatosis; rheumatoid arthritis; psoriasis; bowel disease:
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2000DE-1043826
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                                                                                                                                     ID NO
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                                                                                                                                                                           treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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87.5%;
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ment of diseases
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                     Sequence Listing;
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                                                                                                                                                                          of chemically modified iseases associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
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n abnormal
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences as sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and matrorm part of a set of probes for detecting the cytosine methylation and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specifi
                                                                                                                                                                                                                                                                                                     01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discloses genomic DNA sequences (ABL01840-ABL16175) and (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                  Fragments
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                                                                                                                                                                                                                                                                                                                                                    2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-EP02955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                    NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1049 A; 1020 C;
                                                                                                                                                                                    506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 4654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dinucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.8%;
87.5%;
                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                27pp; English
                                                                                                                                                                                                                                                                                                     Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19.2; D
Pred. No. 2.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oncogene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nt did not form part of the printed
in electronic format directly from
                                                                                                                                                                                                                                                                                                     the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cogene; antitumour;
single-nucleotide |
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  diagnosis
to specific
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                                                                                                                                                                                                                      e.g.
                                                                                                                                                                                                                                              suppressor
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RESULT
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ABL34223/c
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent of the printed specification, but was obtained directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID 2 and ID1 is missing).
                                                                                                                                                                                                                                                               WPI;
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                                                                                                                                          Claim
                                                                                                                                                                              cytosine
                                                                                                                                                                                                 Nucleic acid comprising for diagnosis and treatm
                                                                                                                                                                                                                                                                                                        Olek
                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                              methylation
                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                   Piepenbrock
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2000DE-1043826
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                                                                                                                                        ID NO
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                                                                                                                                                                                               treatment
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                                                                                                                                          2196;
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease; cytosine methylation; antiasthmatic;
antianaemic; cytostatic; nootropic;
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(5)
(4)
                                                                                                                                                                                               fragment of chemically modified gene, use ment of diseases associated with abnormal.
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                                                                                                                                      32pp +
                                                                                                                                                                                                                                                                                                      Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 955 G;
                                                                                                                                    Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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No. 2
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                                                                                                                                        German
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                                                                                                                                                                                                                       useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ce (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo; leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

cancer, acute myeloid

The

invention

provides a number of

human immune system

sequences associated

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ABQ67065/C
ID ABQ670
XX
AC ABQ670
XX
AC ABQ670
DY 28-AUG
DY 28-AUG
XX
HUMAN
XX
HUMAN
KW Inflam
KW macula
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KW antirh
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OS HOMO S
YX
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PN 16-DEC
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PR 06-DEC
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YDI; 'Schach
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer in a particular (d) assessing in a patient; (e) selecting (f) assessing
                                                                                                                                                                                                               angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarterioscierotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule (I) com a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2000;
13-DEC-2000;
  WPI; 2002-500450/53
                                                                                                                                                                                                                                                                                                                                                                                            ABQ67066 standard;
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                              Schacht 0;
                                                                                 06-DEC-2000;
                                                                                                             06-DEC-2001;
                                                                                                                                         13-JUN-2002.
                                                                                                                                                                     WO200246454-A2
                                                                                                                                                                                                                                                                                                          Human angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                      28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patient,
                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasted in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assessing the efficacy of a therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting presence of prostate cancer, stage of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATATATCTACATTAAAAACAA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
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2000US-255281P.
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                                                                                                                                                                                                                                                                                                           associated
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0; Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                                          polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 G;
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2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eic acid molecule (I) comprising (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer
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RESULT 5
ABL05640/
ID ABL0
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determin status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis associated genes (I having sequences (ABQ66917-ABQ67178) or their complements (I), also related oligomers, are used to evaluate the methylation status and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL05640 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                     Claim 1; SEQ ID NO 11402;
                                                                                     New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                              (PEKE
                                                                                                                                                                                                                                                                                                                                pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster expressed
                                                                                                                                                                                                                                                                                                                                                                                                              ABL05640;
                               The invention relates to
                                                                                                                        P-PSDB;
                                                                                                                                                                                                                23-MAR-2000;
                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                          Venter
                                                                                                                                                                                                     11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1823 CATATTTATCTTCATTCAAAACA 1801
                                                                                                                                   2001-656860/75
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                                                                                                                                                                              ) PE CORP NY.
                                                                                                                                                       JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CATATATCTACATTCAAAACA 24
                                                                                                                       ABB61537
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                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                            developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                     2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA; 4025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.2%;
91.3%;
                                                                                                                                                         Ľ
                                                                                                                                                         PWD,
                              an isolated nucleic acid detection
                                                   21pp + Sequence Listing;
                                                                                     detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                           biology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19.8; I Pred. No. 1.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                         Myers
                                                                                                                                                                                                                                                                                                                                                                 polynucleotide SEQ ID NO 11402
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                                                                                                                                                                                                                                                                                                                                           signalling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5474;
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                                                                                      0 or more cell-cell
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capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of

invention

18

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RESULT 2
AAS46772/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
  PRESENTATION OF THE PRESEN
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07-APR-2000;
30-JUN-2000;
  Olek A,
                                                                                                                                                                                                                                                                                                                                                20-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; Cpg dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppressor
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                                                           (EPIG-)
                                                                                                                                                                                                                               15-MAR-2000;
                                                                                                                                                                                                                                                                                     15-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising
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                                                           EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                                                                           2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 17280
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  Berlin K;
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Pred. No. 1.1
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemically modified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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RESULT 3
ABV50732/c
ID ABV50732 standard; cDNA; 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              considered with tumour suppression and concogenes having a sequence taken from 336 (actually 533 since conneces 408, 458 and 500 are missing from the sequence listing) sequences (cs) and sequences complementary to (ss). The nucleic acid may be a complementary to (ss). The nucleic acid may be a complementary to (ss). The nucleic acid may be a complementary to (ss). The nucleic acid may be a complementary to (ss). The nucleic acid may be a complementary to (ss). The nucleotides and may complementary for an extended in an extended in an extended in a complementary for an extended in an extended for ascertaining genetic and/or epigenetic parameters may be compared to another set of genetic and/or epigenetic parameters, the compared to another set of genetic and/or epigenetic parameters, the compared to another set of genetic and/or epigenetic parameters, the compared to another set opening as basis for diagnosis and/or epigenetic parameters which care disadvantageous to patients. The present sequence is one of the complementary sequence of the corresponding odd numbers are the complementary sequence of the corresponding odd numbers sequence (e.g. to be sequence) and IDI, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 22
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cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID 2 and ID1, ID 536 and ID 535, except ior cince is missing).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron format directly from WIPO at format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bases, of a segment of chemically pretreated DNA (CP DNA) e.g. bisulphite, of genes associated with tumour surrestrictions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                    17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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                                                                                                                                                                                                      20-FEB-2001;
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2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; cytostatic;
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Pred. No. 88;
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AAH92498	AAH92497	AAI96618	ABL11307	AAH87775	AAS44850	AAI83128	ABL32987	AAD22327	ABL33590	ABL92276	AAX91990	AAI61372	AAI61371	AAC81914	ABL32034	ABL33023	AAK80686	ABK40051	AAK85579	ABK28210	AAS45373	ABL33425	ABL54360	ABQ54869	AAZ52465	ABA08735	ABQ92010	AAV61483	ABK30312	AAK61674	AAI91681	AAI61518	ABL32062	ABL32705	ABL33519
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## ALIGNMENTS

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Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA
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2708 others
Search completed: July 8, 2003, 04:02:51 Job time: 93.9558 secs
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                                                                                                                                              Query Match 80.8%; Score 20.2; DB 2; Length 140137; Best Local Similarity 88.0%; Pred. No. 2.7e+02; Matches 22; Conservative 0; Mismatches 3; Indels 0;
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86851. .97390
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61966. .68715
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 140137)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13: 100% Sequencing vector: plasmid; 08 Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye: 0% of reads Assembly program: Phrap: version 0.990319 Consensus quality: 128904 bases at least Q40 Consensus quality: 133055 bases at least Q30 Consensus quality: 13365 bases at least Q30 Consensus quality: 135453 bases at least Q20 Consensus quality: 13655 bases at least Q20 Consensus quality: 13656 bases at least Q20 Consensus quality: 13666 bases at least Q20 Consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (30-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 140137) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 122000; agarose-fp
Insert size: 140532; sum-of-contigs
Quality coverage: 3.10 in O20 bases; agarose-fp
Quality coverage: 3.49 in Q20 bases; sum-of-contigs
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Summary Statistics
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* This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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68716
                                                                                                          /note="assembly_name:Contig30"
41916. .47324
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24074. .26703
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contig22"
14613. .17420
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855. .1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/note="assembly_name:Contig33"
56812. .61865
                                   /note="assembly_name:Contig32"
51188. .56711
                                                                         /note="assembly_name:Contig31"
47425. .51087
                                                                                                                                                                                                                         /note="assembly_name:Contig27" 29425. .32886
                                                                                                                                                                                                                                                               vector_side:right"
26804. .29324
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1. .140137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contig17"
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                                                                                                                                                                /note="assembly_name:Contig29"
                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig24
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig21"
|1826. .14512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig19"
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                                                                                                                                                                                                     note="assembly_name:Contig28"
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of 10000 bp
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les 22; Conserv
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Direct Submission

Submitted (23-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Aug 31, 2001 this sequence version replaced gi:13990096. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                        sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA sequence from clone
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                                                                                                                                                                                                                                                              Mammalia;
                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATATATATCTACATTCAAAACAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAAATCGATCTACATTCAAAACAA 18783
                                                                                                                                                                                                                                         karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 114016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER52C repeat: matches 1162.
15276. .15580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLT2D repeat: matches 1. .498 of consensus" 10671. .10960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSg repeat: matches 1. .306 of consensus"
14782. .14909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: Em:AQ358081" 11872. .12194
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10142. .10183
/note="21 copies 2 mer ga 76% con
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9247. .9398
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9433. .9597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MER52C repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSx repeat: matches 1. .304 of
11722. .11767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluJb repeat: matches 3. .275 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluJo repeat: matches 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="AluSp repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                      GI:15384808
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nm clone RP11-338N12 on chromosome
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9, complete
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                                            140137 bp DNA linear h
Homo sapiens chromosome 12 clone RP11-159F8, WORKING
SEQUENCE, 28 unordered pieces.
AC027611
                     AC027611.4 GI:8569832
     HTGS_PHASE1;
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99446 CCATATAGATCTACAAACAAACAA 99470
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                                 1 CCATATATATCTACATTCAAAACAA 25
                                                                                                                                                                         . Similarity 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISSPROT; Tr:, TREMBL; Wighted the conduction of the conduction o
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VECTOR: pBACe3.6
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                                                                                                                                                                              Conservative
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61961. .6203
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/note="Sequence from overlapping clone RP11-366H6
(AL449304). Assembly confirmed by restriction digest."
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/note="Sequence from overlapping
(AL449304) Assembly confirmed by
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/note="Sequence from overlapping clone RP11-366H6
(AL449304). Assembly confirmed by restriction digest."
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/note="Sequence from overlapping clone RP11-366H6
(AL449304). Assembly confirmed by restriction diga
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                                                                                                                                                                                                                     Score 20.2; DB 9; Pred. No. 2.8e+02;
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restriction digest."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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RP11-264M3 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at
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true left end of clone RP11-74J13 is at 25440 in this sequence. true right end of clone RP11-2P5 is at 100 in this sequence.
                                                                                                                 /note="39 copies 2
5712. .6012
                                                                                                                                                                                                                                                                                                                                                    /note="L1PA11 repeat: matches 4058. .5306 of consensus" 4487. .4660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluSc repeat: matches 1. .303 of consensus" 1886. .2614
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                                                                6014.
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/db_xref="taxon:9606"
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      /note="AluSx repeat: matches 1. .133 of consensus"
5161. .6531
                                                                /note="AluY repeat: matches 1.
5014. .6148
                                                                                                                                                                                                       'note="Alusx repeat: matches 127. .299 of
                                                                                                                                                                                                                                                                                                               /note="MER50 repeat: matches 553.
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"17 copies 2 mer tt 88% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L1PA11 repeat: matches 6054.
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                                                                                                                                               ta 85% conserved
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complement(8816. .8994)
/note="match: GSS: Em:AQ527616"
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6533. .6754
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/note="match: STS:
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complement(8807. 9429)
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                                                                                                                                                                                                                                                                                  complement(8970.
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/note="Alus
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complement(9133
/note="match: G!
                                                                                                                                                                                                                       complement(8982
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/note="match: GS
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/note="LTR39 repeat: matches 410. .609 of consensus"
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                                                                        /note="match:
9124. .9432
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/note="match: GSS:
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/note="43 c
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/note="match: GSS: Em:AZ380835"
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                          /note="match: GSS: Em:AQ788085"
                                            /note="AluSg repeat: matches 1.
complement(9125. .9426)
                                                                                                      complement(9100
                                                                                                              3021. 9076
/note="28 copies 2 mer at 73% conserved"
                                                                                                                                             1020. .9121
note="match: GSS:
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/note="match:
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775. 9093)
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                                                                                      Em: AQ782185°
                                                                                                                                              Em: AZ396895"
                                                                                                                                                                             Em: AQ083235'
                                                                                                                                                                                                                                                                   西m:G45335"
                                                                                                                                                                                                                                                                                                                            Em: AQ077299'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Em: AZ254467"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Em: AQ781128"
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                                                                                                                                                                                                         Em: AZ458983"
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Em: AQ178343'

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RESULT 11
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 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus chromosome UNX clone
SEQUENCE, 5 unordered pieces.
AC122828
AC122828.1 GI:21206486
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990319
Consensus quality: 268408 bases at least Q40
Consensus quality: 269116 bases at least Q30
Consensus quality: 269568 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Veri
Mammalia; Eutheria; Rodentia; Sciurognathi;
1 (bases 1 to 270987)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 195000; agarose-fp
Insert size: 270587; sum-of-contigs
Quality coverage: 18.59 in Q20 bases; agarose-fp
Quality coverage: 10.33 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; 0% Sequencing vector: Blasmid; 100% Chemistry: Dye-primer ET; 0% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 270987)
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: M_BA0215B08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
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                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                          1473
1573
2811
2911
                                     /db_xref="taxon:10090"
/chromosome="UNK"
                                                                       /organism="Mus musculus"
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               /clone="RP23-215B8"
                                                                                                             ocation
                                                                                                                      1472: contig of 1472 bp in length
1572: gap of unknown length
2810: contig of 1238 bp in length
2910: gap of unknown length
47530: contig of 44720 bp in length
47730: gap of unknown length
107746: contig of 60016 bp in length
107846: gap of unknown length
107846: gap of unknown length
270987: contig of 163141 bp in length
                                                                                             .270987
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                                                                                                             Qualifiers
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TITLE
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ORGANISM
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VERSION
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AX251530/c
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262929 TATATATCTACATTCAAAAGAA 262950
Direct Submission
Submitted (25-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 13., UK. E-mail enquiries: humquery@sanger.ac.uk Clone Cequests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      artificial sequences.

1 (bases 1 to 17280)

Olek, A., Piepenbrock, C. and Berlin, K.
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Sequence 498 from Patent W00168912.
AX251530
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21; Conservative
                                                                                                                                                                                                                                                      Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           . Similarity 22; Conserv
                                                                                                                                                                                                                        sequence. AL161775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct.
                                                                                                                      Mammalia;
                                                                                                                                      Eukaryota;
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                      AL161775.20
                                                                                                                                                                                                                                                                        AL161775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent:
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                                                                                     Lovell, J
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107847. .270987
/note="assembly_name:Contig9"
s 56456 c 54330 g 79404 t
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2911. 47630
/note="assembly_name:Contig7"
47731. 107746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig5"
1573. .2810
                                                                                                   ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 to 25539)
                                                                                                                                                                                                                                                      25539 bp DNA linear PRI 25 sequence from clone RPI1-264M3 on chromosome 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="chemically treated genomic 151 c 3624 g 8775 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/db_xref="taxon:32630"
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Pred. No. 1.9e
0; Mismatches
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Pred. No. 4.1e+02;
0; Mismatches 3;
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hes 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Gilde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hilme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Menenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trajillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 226726)

Tander, E., Ali, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 226726)
Birren,B., Linton,L., Nusbaum, on Mus musculus, clone RP23-28P10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Boukhgalter,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                               Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 26, 2002 this sequence version replaced gi:21536040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                               Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 226726)
  Center project name: 2
                                                   ----- Project Information
                                                                             Contact: sequence_submissions@genome_wi.mit.edu
                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                    Center code: WIBR
                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                        Submission
                                                                                                                                                                                                                                                                                                                                                                                                               Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Lander, E
Query Match
Best Local Similarity
Thes 21; Conserve
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the accession number will be preserved.

1 1496: contig of 1496 bp in length
1497 1596: gap of 100 bp
1853: contig of 257 bp in length
1854: 1953: gap of 100 bp
1954: 5276: contig of 3733 bp in length
5277: 5376: gap of 100 bp in length
5277: 5376: gap of 100 bp in length
9085: 9184: gap of 100 bp
9185: 25659: contig of 16475 bp in length
25760: 25759: gap of 100 bp
25760: 25759: gap of 100 bp
48398: 48499: gap of 100 bp
48398: 48499: gap of 100 bp
48398: 48499: gap of 100 bp
48498: 144109: contig of 25638 bp in length
48498: 144109: contig of 95612 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 240000; agarose-fp Insert size: 225926; sum-of-contigs Quality coverage: 7.9 in Q20 bases; quality coverage: 8.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 224168 bases at least Q40 Consensus quality: 225210 bases at least Q30 Consensus quality: 225616 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144110 144209: gap of 100 bp
144210 200142: contig of 5593 bp in length
200143 200242: gap of 100 bp
200243 226726: contig of 26484 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
48498. 144100
                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
25760. .48397
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
5377. .9084
                                                                                          vector_side:right"
. 45772 c 45704 g
                                                                                                                                              clone_end:T7
                                                                                                                                                                200243. .226726
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_end:SP6
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/clone="RP23-28P10"
                                                                                                                                                                                                                    /note="assembly_fragment"
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144210. .200142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment
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81.6%;
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Score 20.4; DB : Pred. No. 2e+02;
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                    2;
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                                                                                                  800 others
                    Length 226726;
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